

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 176372

TO: Konstantina Katcheves Location: REM-2A60/2C70

Art Unit: 1636

Friday, January 20, 2006

Case Serial Number: 10/511327

From: Barb O'Bryen

Location: Biotech-Chem Library

Remsen 1a69

Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

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AY781400 Synthetic AY7881400 Synthetic AY738638 Cloning v AY738638 Cloning v M12545 Synthetic g M15949 Synthetic g AR084419 Sequence BD073246 In vitro AR353866 Sequence AR084418 Sequence AR084418 Sequence AR084418 Sequence AR084418 Sequence AR084418 Sequence AR084418 Sequence M13653 Bacteriopha AV2708 phwso6 DNA M35371 E.coli DNA AR084426 Sequence AR084426 Sequence AR084426 Sequence AR084426 Sequence AR08377 Bacteriop
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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Synthetic construct transposon mini-Mu transposon TnCR6, complete
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Pred. No. 0.00055;
0; Mismatches 7; Indels 0;
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Submitted (14-077-2004) CopyRat Pty Ltd,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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1 (bases 1 to 1319)
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                     AY738638
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SYNGENE
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AR084420
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BD073246
AR353866
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Best Local Similarity 87.0%;
Matches 47; Conservative (
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(without alignments)
11032.288 Million cell updates/sec
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           GenCore version 5.1.6
(c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gaps

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Result Š. 54

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Gaps

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Indels

Length 1351;

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87.0%;
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Synthetic construct transposon mini-Mu transposon TnCR7, complete
sequence.
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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1 (bases 1 to 1351)
Zhang,C., Kitsberg,D., Chy,H., Zhou,Q. and Morrison,J.R.
Transposon-mediated generation of targeting vectors for production of gene knockouts

(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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Pred. No. 0.00055;
); Mismatches 7; Indels 0;
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DEFINITION
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SYN 28-FEB-2005
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1351 bp DNA linear SYN 28-FEB-200 construct transposon mini-Mu transposon TnCR7, complete
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
                                                                                                                                                                                                                                                                                                           Zhang, C., Kitsberg, D., Chy, H., Zhou, Q. and Morrison, J.R. Transposon-mediated generation of targeting vectors for the production of gene knockouts (er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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87.0%; Pred. No. 0.00055;
cive 0; Mismatches 7; Indels 0;

    1351
/organism="synthetic construct"

                                                                                                                                                                                                                                                other sequences; artificial sequences.
1 (bases 1 to 1351)
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Query Match 79.3
Best Local Similarity 87.0
Matches 47; Conservative
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FPIMQLVGQVPAALWVIFGEDRFRWSATWIGLSLAVFGILHALAQAFVTGPATVRFGE
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QLQGSLAALTSLTSITGPLIVTAIYAASASTWNGLAWIVGAALXLVCLPALRRGAWSR
ATST
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RIVAGITGATGAVAGAYIADITDGEDRARHFGLMSACFGVGMVAGPVAGGLLGAISLH
                                                                                                                               SYN 28-FEB-2005
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Synthetic construct transposon mini-Mu transposon TnCR4, complete
                                                                                                                             AY781401 1524 bp DNA linear SYN 28-FEB-200
Synthetic construct transposon mini-Mu transposon TnCR4, complete
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                     1350 GATCTGAAGCGGCGCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGGAAAAC 1297
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other sequences; artificial sequences.
I (bases 1 to 1524).
Zhang,C., Kitebers,O., Chy,H., Zhou,Q. and Morrison,J.R.
Transposon-mediated generation of targeting vectors for the
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/db_xref="G1:60171910"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transposon="mini-Mu transposon InCR4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="synthetic construct"
/mol_type="other DNA"
/db_xref="taxon:32630"
1. .1524
                                                                                                                                                                                                                                                                            other sequences; artificial sequences.
1 (bases 1 to 1524)
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APFLAAAVLNGLNLLLGCFLMQESHKGERRPMPLRAFNPVSSFRWARGMTIVAALMTV
FFINQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGE
KARII SAGMAADALGYVLLAFATRGWMAFPINILLASGGIGMPALQAMLSRQVDDDHQG
QLQGSLAALITSLTSITGPLIVTAIYAASASTWNGLAWIVGAALYLVCLPALRRGAWSR
ATST"
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Synthetic construct transposon mini-Mu transposon TnCR1, complete
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
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1 (bases 1 to 1808)
Zhang,C., Kitsberg,D., Chy,H., Zhou,Q. and Morrison,J.R.
Transposon-mediated generation of targeting vectors for the production of gene knockouts
(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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|codon start=1
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production of gene knockouts
(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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1. 1524
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1. 1808
/transposon="mini-Mu transposon TnCR1"
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Location/Qualifiers
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87.0%;
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ANMDNFPAPVFTMGKYYTQGBKULMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
A"
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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LKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIMDSVHPCYTVFHÈQTETF
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Synthetic construct transposon mini-Mu transposon TnCR1, complete
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Direct Submission
Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street, Clayton, Victoria 3168, Australia
Location/Qualifiers
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1 (bases 1 to 1808)
Zhang,C., Kitsberg,D., Chy,H., Zhou,Q. and Morrison,J.R.
Transposon-mediated generation of targeting vectors for the production of gene knockouts
(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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                                                                                                                                                        79.3%; Score 42.8; DB 11; Length 1808;
.larity 87.0%; Pred. No. 0.00053;
Conservative 0; Mismatches 7; Indels 0;
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Pred. No. 0.00053;
0; Mismatches 7; Indels 0;
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87.0%;
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AY781403 1937 bp DNA linear SYN 28-FEB-2005 Synthetic construct transposon mini-Mu transposon ThCR5B, complete

DEFINITION

AY781403 LOCUS

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/trānslation="MIEQDGLHAGSPAAWVBRLFGYDWAQQTIGGSDAAVFRLSAQGR
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lsshlapaekvsimadamrrlhtldpatcpfdhoakhrierartrmeaglvdoddlde
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Synthetic construct transposon mini-Mu transposon TnCR5B, complete
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                                                                                                                                                            Zhang, C.
Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
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Direct Submission
Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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1. 1937
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87.0%; Pred. No. 0.00053;
ative 0; Mismatches 7;
                                                                                                             other sequences; artificial sequences [1 (bases 1 to 1937)
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AY781403.1 GI:60171960
                   AY781403.1 GI:60171960
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QDIALATRDIAEELGGEWADRPLVLYGIAAPDSQRIAFYRLLDEFF"
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Synthetic construct transposon mini-Mu transposon TnCR8B, complete
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Synthetic construct transposon mini-Mu transposon TnCR8B, complete
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Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street, Clayton, Victoria 3168, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     Zhang,C., Kitsberg,D., Chy,H., Zhou,Q. and Morrison,J.R. Transposon-mediated generation of targeting vectors for the production of gene knockouts
(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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                                                         Query Match 79.3%; Score 42.8; DB 11; Length 1937; Best Local Similarity 87.0%; Pred. No. 0.00053; Matches 47; Conservative 0; Mismatches 7; Indels 0;
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/mol_type="other DNA"
/db_xref="taxon:32630"
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1 (bases 1 to 2037)
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AY781407.1 GI:60172085
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Synthetic construct transposon mini-Mu transposon TnCR5A, complete
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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other sequences; artificial sequences.

(bases 1 to 2037)
Zhang,C., Kitsberg,D., Chy,H., Zhou,Q. and Morrison,J.R.
Transposon-mediated generation of targeting vectors for production of gene knockouts
(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
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1. .2062
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644. .1438
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    .2037
/organism="synthetic construct"

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1. .2037
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synthetic construct
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EHQGLAPAELPARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDCGRLGVADRY
QDIALATRDIAEELGGEWADRPLVLYGIAAPDSQRIAFYRLLDEFF"
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Synthetic construct transposon mini-Mu transposon TnCRBA, complete
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Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 2162)
2 Shang,C., Kitsberg,D., Chy,H., Zhou,Q. and Morrison,J.R.
Transposon-mediated generation of targeting vectors for the
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Pred. No. 0.00052;
0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other sequences, artificial sequences.
1 (bases 1 to 2062)
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1 Similarity 87.0%;
47; Conservative
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synthetic construct
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Best Local Similarity
Matches 47; Conserva
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AY781406
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KEYWORDS
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EHQGLAPAELFARLKARMPDGEDLVVTHGDACLPNIMVENGRFSGFTDGGRLGVADRY
QDIALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
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                                                                                                                Zhang,C.
Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
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production of gene knockouts
(er) Nucleic Acids Res. 33 (3), E24 (2005) In press
15699181
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769. .1563
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AB68984
ADR85691
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              AAZ28877
AAD01008
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AAS98204
ADS73196
ADW42050
ABL70342
AAS61297
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              GenCore version (c) 1993 - 2006
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                                                                      nucleic search, using sw model
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Minimum DB Maximum DB

Database

Result Š.

Searched:

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Indels

Length 1254;

100.0%; Score 54; DB 10; 100.0%; Pred. No. 8.2e-10; 0; Mismatches

Query Match Best Local Similarity 100. Matches 54; Conservative

54 54

GATCTGATTGATTGAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC

BP.

ACF58169 standard; DNA; 1254

RESULT 3 ACF58169/c

ds.

Transposon; genetic engineering; transposase; Cat-Mu;

Synthetic. Bacteriophage mu. WO2003087370-A1.

Modified Cat-Mu(Stop)-transposon.

(first entry)

15-JAN-2004

ACF58169;

1 GATCTGATTGATGGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC

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genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of a transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence recognized by a transposase, and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a Cat-Mu transposon modified end
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5.3e-10;
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Pred. No.
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Matches 54
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14-APR-2003; 2003WO-FI000285. 18-APR-2002; 2002FI-00000746.

23-OCT-2003

Savilahti H, Tieaho V; (FINN-) FINNZYMES OY

WPI; 2003-845329/78.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by transposase useful for producing deletion derivatives of polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 54; DB 10; Length 1254; 100.0%; Pred. No. 8.2e-10; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1254 BP; 356 A; 296 C; 264 G; 338 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 30; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACF58172 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
tes 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ID ACF5
XX
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g
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genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid acid containing a polypeptide coding nucleic acid and in the presence of a transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end acid having the transposon incorporated in the protein coding nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a modified Cat-Mu(Stop)-transposon

Sequence 1254 BP; 356 A; 296 C; 264 G; 338 T; 0 U; 0 Other;

The invention relates to a transposon nucleic acid comprising a

Claim 6; Page 30; Opp; English.

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The present invention relates to a method for making an insertional mutation at a random or quasi-random position in cellular nucleic acid in a target cell comprising introducing into the target cell a synaptic complex. The method is particularly useful for efficiently inserting a transposable polynucleotide at random or quasi-random locations in the chromosomal or extra-chromosomal nucleic acid of a target cell. The method may also be used for screening the genome of cells that comprise an insertional mutation that induces a phenotypic or genotypic change relative to the cells that are not subject to insertional mutagenesis. The present sequence is the precut transposon end of Bacteriophage Mu non-transferred strand, used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .4
/taga a
/note= "the 5' end of this strand overhangs the 3'end of
the complementary strand"
                                                                                                                                                                                                                                                               Making an insertional mutations, especially useful for efficiently inserting a transposable polynucleotide in a target cell, comprises introducing into the target cell a synaptic complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCTGAAGCGGCGCACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATCTGATTGATTGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transposon; genetic engineering; transposase; Cat-Mu; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54 BP; 21 A; 12 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.3%; Score 42.8; DB 4;
87.0%; Pred. No. 6.4e-06;
Live 0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cat-Mu transposon containing wild-type Mu ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Claim 6; Col 2; 11pp; English.
                                                                                                                               (WISC ) WISCONSIN ALUMNI RES
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                                            10-AUG-2000; 2000US-00635969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-2003; 2003WO-FI000285
                                                                                        98US-00159363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACF58170 standard; DNA; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FINN-) FINNZYMES OY
                                                                                                                                                                                                                       WPI; 2001-656171/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage mu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003087370-A1
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                                                                                        23-SEP-1998;
                                                                                                                                                                             Goryshin IY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc feature
  25-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACF58170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a transposon nucleic acid comprising a genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence in containing a transposase; and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a Cat-Mu transposon modified end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized transposase useful for producing deletion derivatives of polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Precut transposon end of Bacteriophage Mu non-transferred strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGATTGATTGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGATTGATTGAACGAAAAACGCGAAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                    Transposon; genetic engineering; transposase; Cat-Mu; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50 BP; 21 A; 8 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%; Score 50; DB 10; 100.0%; Pred. No. 1.5e-08; ive 0; Mismatches 0;
                                                                                        Cat-Mu transposon modified end fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 31; Opp; English.
                                                                                                                                                                                                                                                                                                                                    14-APR-2003; 2003WO-FI000285.
                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002; 2002FI-00000746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid. The present sequence re
fragment without 5' overhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD21279 standard; DNA; 54
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteria phage Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Savilahti H, Tieaho V;
                                                                                                                                                                                                                                                                                                                                                                                                                          (FINN-) FINNZYMES OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845329/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                  Bacteriophage mu.
                                                                                                                                                                                                                                            WO2003087370-A1.
                                            15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6294385-B1
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28-JAN-2002
                                                                                                                                                                                                                                                                                        23-OCT-2003
                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD21279;
ACF58172;
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RESULT 5 AAD21279

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                                                                                                                                                                                                                                                            genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid at containing a polypeptide coding nucleic acid and in the presence of a transposon concaining a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence recognized by a transposase; and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a Cat-Mu transposon containing wild
                                                                                                         by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant and/or animal genome in a predetermined way.
                                                                                                      translation stop signal within a transposon end sequence recognized l
transposase useful for producing deletion derivatives of polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector; transposon; recombination; genome; primer; PCR; ss.
                                                                          transposon nucleic acid comprising a genetically engineered
                                                                                                                                                                                                                                      The invention relates to a transposon nucleic acid comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATCTGATTGATTGAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCTGAAGCGGCGCACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.8; DB 10; Length 54;
Pred. No. 6.4e-06;
0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 54 BP; 21 A; 12 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Page 51; 92pp; English.
                                                                                                                                                                                       Example 4; Fig 2; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 construct; targeting
plant genome; animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-2001; 2001AU-00008174.
23-MAY-2002; 2002AU-00002522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-OCT-2002; 2002WO-AU001367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC80745 standard; DNA; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COPY-) COPYRAT PTY LTD
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                      WPI; 2003-845329/78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Targeting deletion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC80745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
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The invention relates to methods of preparing a targeting construct for use in a targeting vector capable of modifying a target DNA sequence, by obtaining a copy of the target DNA sequence in vitro, inserting a DNA

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sequence comprising a transposon sequence and a DNA recombination sequence at two sites in the copy of the target DNA sequence, and inducing a recombination event between the recombination sequences to delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target construct for use in a targeting vector for gene targeting or homologous recombination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targeting construct; targeting vector; transposon; recombination;
                                                                                                                                                                                                                                                                                                                                                                                         GATCTGAAGCGGCGCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                           1 GATCTGATTGATTGAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transposon-based targeting construct related primer Mu1-4.
                                                                                                                                                                                                                                                                        DB 10; Length
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      deletion; plant genome; animal genome; primer; PCR; ss.
                                                                                                                                                                                                                               Sequence 82 BP; 35 A; 21 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83 BP; 29 A; 20 C; 18 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        Score 42.8; DB 10;
Pred. No. 6.8e-06;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence, useful in making a targeting vecto and/or animal genome in a predetermined way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 42.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 50; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC80741 standard; DNA; 83 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-2002; 2002WO-AU001367.
                                                                                                                                                                                                                                                                        79.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2001; 2001AU-00008174.
23-MAY-2002; 2002AU-00002522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COPY-) COPYRAT PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-393445/37.
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003031629-A1
                                                                                                                                                                                                                                                                                                                      47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morrison J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC80741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
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construct; targeting vector; transposon; recombination; plant genome; animal genome; primer; PCR; 88.

15-OCT-2003

Targeting

(COPY-) COPYRAT PTY LTD

17-APR-2003

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The invention relates to methods of preparing a targeting construct for use in a targeting vector capable of modifying a target DNA sequence, by obtaining a copy of the target DNA sequence in vitro, innerting a DNA sequence and user, into, innerting a DNA sequence and a DNA recombination sequence comprising a transposon sequence and a DNA recombination sequence, and inducing a recombination event between the recombination sequence, and delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target recompositions of the present invention are useful for preparing a target recompination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant and/or animal genome in a predetermined way.
                                                                             Transposon-based targeting construct related primer Mu2-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 50; 92pp; English.
                                                                                                                                                                                                                                                                                                                                             08-OCT-2002; 2002WO-AU001367.
                                                                                                                                                                                                                                                                                                                                                                                            09-OCT-2001; 2001AU-00008174.
23-MAY-2002; 2002AU-00002522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrison J, Zhang C;
                                                                                                                                                                                                                                                WO2003031629-A1.
                                                                                                                                                                                                   Synthetic.
                                                                                                                                                   deletion;
          g
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                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to methods of preparing a targeting construct for obtaining a copy of the target DNA sequence in vitro, inserting a DNA sequence, by obtaining a copy of the target DNA sequence in vitro, inserting a DNA sequence comprising a transposon sequence and a DNA recombination sequence at two sites in the copy of the target DNA sequence, and inducing a recombination event between the recombination sequences to delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target construct for use in a targeting vector for gene targeting or homologous recombination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant and/or animal genome in a predetermined way.
                                Gaps
                                                                             54
                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeting construct; targeting vector; transposon; recombination; deletion; plant genome; animal genome; primer; PCR; ss.
                                                                                                         GATCTGAAGCGGCGCACGAAAAAGCGCGAAAGCGTTTCACGATAAATGCGAAAAAC
                                                                             1 GATCTGATTGAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 84;
                                                                                                                                                                                                                                                                                                                                                                                            construct related primer Mul-1.
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 84 BP; 29 A; 20 C; 19 G; 16 T; 0 U; 0 Other;
       Pred. No. 6.8e-06;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.8; DB 10
Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 50; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-2001; 2001AU-00008174.
23-MAY-2002; 2002AU-00002522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-2002; 2002WO-AU001367
     87.0%;
                                                                                                                                                                                                                                                ACC80738 standard; DNA; 84
                                                                                                                                                                                                                                                                                                                                                                                            Transposon-based targeting
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.0°
Matches 47; Conservative
                              47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COPY-) COPYRAT PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-393445/37.
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003031629-A1.
                                                                                                                                                                                                                                                                                                                                             15-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morrison J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                             ACC80738
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                                                       Gaps
                                                                                54
                                                                                                           64
                                                                                                                                                                                                                                                                                                Targeting construct; targeting vector; transposon; recombination; deletion; plant genome; animal genome; primer; PCR; ss.
                                                                                  1 GATCTGATTGAATGAAAAACGCGAAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                     GATCTGAAGCGGCGCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAAC
                                                      ;
0
                                                                                                                                                                                                                                                                     Transposon-based targeting construct related primer Mu-polyA-2.
                           DB 10; Length 86;
                                                      Indels
Sequence 86 BP; 27 A; 20 C; 20 G; 19 T; 0 U; 0 Other;
                                         Pred. No. 6.8e-06;
0; Mismatches 7;
                          79.3%; Score 42.8;
87.0%; Pred. No. 6.
                                                                                                                                                                                   ACC80753 standard; DNA; 89
                                                                                                                                                                                                                                           15-OCT-2003 (first entry)
                                                       Conservative
                                         Local Similarity
les 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                     WO2003031629-A1
                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-2003
                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                               ACC80753;
                             Query Match
                                                       Matches
                                                                                                                                                         RESULT 11
                                                                                                                                                                       ACC80753
                                                                                                                                                                                   BXBXSXXXXXXXXXXXXXX
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Gaps

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7; Indels

0; Mismatches

54

GATCTGAAGCGGCGCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 64

11

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ACC80742 standard; DNA; 86

RESULT 10 ACC80742 ID ACC8 XX AC ACC8

ACC80742

1 GATCTGATTGAATGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC

Brack Strain

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The invention relates to a transposon nucleic acid comprising a genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of a transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence recognized by a transposase, and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a modified Cat-Mu transposon containing Mu ends with engineered NotI restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a mismatch in a test double stranded nucleic acid target, useful for typing a pathogenic microorganism strain, comprises detecting transposition of the Mu-end nucleic acid into the target.
                                                                                      New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by transposase useful for producing deletion derivatives of polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of detecting a mismatch in a test double stranded nucleic acid target which comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; mismatch detection; transposition detection; pathogen typing; embryo screening; mutation detection; Mu end DNA; MM1141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GATCTGATTGATTGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATCTGCGGCCGCGCACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mu end DNA fragment construction oligonucleotide MM1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54 BP; 19 A; 14 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41.2; DB 10,
Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 2; 24pp; English.
                                                                                                                                                                                Example 4; Fig 2; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2004; 2004US-00809688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-2003; 2003US-0457934P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.3%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
Savilahti H, Tieaho V;
                                             WPI; 2003-845329/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence comprising a transport on a sequence and a DNA recombination sequence of transports on the copy of the target DNA sequence, and inducing a recombination event between the recombination sequences to delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target construct for use in a targeting vector for gene targeting or homologous recombination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
                                                                                                                                                                                                                                                                    Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant and/or animal genome in a predetermined way.
                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to methods of preparing a targeting construct for use in a targeting vector capable of modifying a target DNA sequence, by obtaining a copy of the target DNA sequence in vitro, inserting a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= a
note= "the 5' end of this strand overhangs the 3'end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATCTGATTGATTGAACGAAAAACGCGAAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 GATCTGAAGCGGCGCACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transposon; genetic engineering; transposase; Cat-Mu; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 89 BP; 28 A; 19 C; 20 G; 22 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.8; DB 10
Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cat-Mu(NotI) transposon modified end fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the complementary strand'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 52; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACF58171 standard; DNA; 54 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002FI-00000746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%;
                08-OCT-2002; 2002WO-AU001367.
                                                              09-OCT-2001; 2001AU-00008174
23-MAY-2002; 2002AU-00002522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-APR-2003; 2003WO-FI000285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                   (COPY-) COPYRAT PTY LTD.
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′*tag≕
                                                                                                                                                                              Zhang C;
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                                                                                                                                                                                                                              WPI; 2003-393445/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003087370-A1
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                                                                                                                                                                              Morrison J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACF58171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches

RESULT 12

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Gaps

ö 54;

Indels

8

DB 10; Length

54 54 Sequence 56 BP; 22 A; 12 C; 15 G; 7 T; 0 U; 0 Other;

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transposition of the Mu-end nucleic acid into the target, where transposition at the predominant site indicates the presence of mismatch at about that site. The methods are useful for typing a pathogenic microorganism strain, for screening an embryo for the presence of mutation, for detecting the presence of known mutation in a gene of interest, detecting the presence of a previously unidentified mutation in a gene of interest, and diagnosing the presence or absence of a tumourpromoting mutation. The kit is useful for detecting the presence of a mutation or polymorphism of interest in a nucleic acid molecule. The present sequence represents the Mu end DNA fragment construction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a mismatch in a test double stranded nucleic acid target, useful for typing a pathogenic microorganism strain, comprises detecting transposition of the Mu-end nucleic acid into the target.
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; mismatch detection; transposition detection; pathogen typing; embryo screening; mutation detection; Mu end DNA; MM1138.
                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                              73.0%; Score 39.4; DB 13; Length 51; larity 97.6%; Pred. No. 0.00011; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end DNA fragment construction oligonucleotide MM1138.
                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                         42 GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 2
                                                                                                                                                                                                                                                     Sequence 51 BP; 6 A; 13 C; 11 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                 14 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 1; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS13820 standard; DNA; 56 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2004; 2004US-00809688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2003; 2003US-0457934P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanagihara K, Mizuuchi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                oligonucleotide MM1141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteria phage Mu
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                                                                                                                                                                                                                                                                                                               Local Similarity
nes 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004191821-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a Mu-like transposable element (1) used for generating functional fusion proteins after insertion into a target DNA. The Mu-like element comprises: (a) a left transposable element attachment site atts and a right transposable element attachment site attR. where attR is no more than 62 nucleotides long; (b) a site for insertion of an exogenous DNA sequence encoding for a protein domain located between attL and attR; (c) after insertion of the transposable element into a target DNA sequence, a fusion mRNA sequence is transcribed originating either from the target DNA on either side of the transposable element or from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating fusion proteins using transposable elements, useful for development of a protein domain library and in the construction of multi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inside the transposable element and continuing through the attachment site sequences and into the protein coding region, resulting in a single fusion open reading frame (OFF). The constructs are useful in the development of a protein domain library, in the construction of multi-
                                                                                                                                                                                                                                                                                                                                       Transposon Mu; transposable element; fusion protein; attachment site; attL; attR; protein domain library; enzyme; accelerated evolution; 88
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  functional enzymes and in the accelerated evolution of new enzymatic activities. The sequences AAZ28880-Z28884 represent deletion mini-Mu elements of the invention (encoded ORF - AAY55901-Y55906)
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     26;
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     Length
                                        Indels
                                                                                           14 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 54
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                                                                                                                                                                                                                                                                                                     Mini-Mu transposable element deletion region delta-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaines GL;
 Score 39.4; DB 13,
Pred. No. 0.00011;
0; Mismatches 1;
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 73.0%;
97.6%;
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                                                                                                                                                                                               AAZ28883 standard; cDNA; 58
                                                                                                                                                                                                                                                                  15-FEB-2000 (first entry)
                                      Conservative
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CASADABAN M J.
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Query Match
Best Local Similarity
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                                        40;
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49 GCACGAAAAACGCGAAAAGCGTTTCACGATAAATGCGAAAAAC 9

Search completed: January 17, 2006, 19:35:05 Job time: 35.5794 secs

283PvD05 DKFZp434L 603056184 AGENCOURT HVSMEm001

BI953931

BQ149276 NF088008F B1953878 HVSMEm001 DU005263 300893 TO AZ152875 SP 0046 B CJ193910 CJ7399910 CJ417250 CJ417250 B1953959 HVSMEm001 CNS66362 USDA-FP 1 CF564687 USDA-FP 1 DN797614 USDA-FP 7 BR64386 BOHXPB-FP 7 BR64386 BOHXPB-FP 7 BR64389 CH240 222 BW085322 BW085322 BM617600 170006871 B1553998 HVSMEm001 CCS22852 USCKS011_0

Perfect score:

Run on:

Sequence:

Scoring table:

Database

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza brachyantha
Oryza brachyantha
Oryza brachyantha
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
I (bases 1 to 370)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudran,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08 Ba0003F02.r OB Ba Oryza brachyantha genomic clone OB Ba0003F02 3', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fal: 520 629 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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BACKWARD: CAC TCA TTA GGC ACC CCA
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Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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PCR PRimers
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AZ152875
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BM804853
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RESULT 1
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LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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CZ821413 OC Ba019
CZ821717 OC Ba019
CZ821771 OC Ba019
BJ016030 BJ016030
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B1954000 HVSMBm001
P05165 HSC02H021 I
P05165 HSC02H021 I
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Listing first 45 summaries
                                                                                                       OM nucleic - nucleic search, using sw model
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 589)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Joetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
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Oryza coarctata
Oryza coarctata
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
I bases I to 843
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,
Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
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Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Pax: 520 621 1259
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                                                                                                                                                                                                                                           OMAP project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Pers: 520 621 1259
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0089 row: D column: 12
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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PCR PRimers
FORWARD: TAA TAC GAC TCA CTA TAG GG
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PCR PRimers
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Best Local Similarity 97.6%
Matches 40; Conservative
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CZ821413
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                                                                                        Gaps
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/lab_host="DH10B"
/clone_lib="zMMBBb"
/note="wector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Zea mays L. ssp. mays"
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                   Query Match 74.8%; Score 40.4; DB 10; Length 370; Best Local Similarity 97.6%; Pred. No. 0.00042; Matches 41; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 0115 row: J column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing of the maize genome Unpublished (2003) Contact: Rod Wing Arizona Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: BAC ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence.
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CC742071.1 GI:32194524
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Oryza rufipogon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: M13r
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CZ821171 247 bp DNA linear GSS 26-JUL-2005 OC Ba0199J21.r OC Ba Oryza coarctata genomic clone OC Ba0199J21 3', genomic survey sequence.
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| Jab_host="DHIOB"
| clone lib="OC Ba"
| /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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BJ016030 MF01SSA cDNA Oryzias latipes cDNA clone MF01SSA008A02 3',
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 247)
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
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Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OWAP (Oryza Map Alignment Project) - Arizona Genomics Institute Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
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3; Indels
                                     Oryza coarctata (Porteresia coarctata)
Oryza coarctata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xxef="taxon:77588"
/clone="OC_Ba019921"
/tissue_type="leaves"
Mismatches
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Plate: 0199 row: J column: 21
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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38; Conservative
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BJ016030
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OC_Ba0199D21.r OC_Ba Oryza coarctata genomic clone OC_Ba0199D21
3', genomic survey sequence.
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/lab_host="DH10B"
/clone_lib="OC_Ba"
/note="Vector: pAGIBAC1; Site_l: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                        /clone lib="OC_Ba"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
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Oryza coarctata
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
I (bases I to 68)
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
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                                                                                                                                                                                                                                                                                                                                                         67.0%; Score 36.2; DB 10; Length 543; 92.7%; Pred. No. 0.014; live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.0%; Score 36.2; DB 10; Length 688; 92.7%; Pred. No. 0.014;
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
TE1: 520 629 9595
Fax: 520 621 1259
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                                                                           Location/Qualifiers
1. 543
/organism="Oryza coarctata"
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/organism="Oryza coarctata"
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0199 row: D column: 21
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
             Plate: 0199 row: P column: 13
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
SACKWARD: CAC TCA TTA GGC ACC CCA
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/db_xref="taxon:77588"
/clone="OC_Ba0199D21"
/tissue_type="leaves"
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PCR PRimers
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                                                                                                                                                                                                                                /dev_stage="mature"
/lab_host="DH10B"
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Best Local Similarity 92.7%
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Best Local Similarity
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OMAP (O)
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VERSION KEYWORDS SOURCE ORGANISM

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Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Booideae; Triticeae; Hordeum.
I (bases I to 75),
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Oates, R. and Main, D.
Bovelopment of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
                                        1 (bases 1 to 582)
Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H.
Medaka EST Project in Takeda's lab
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias. 1 (bases 1 to 582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 GTIGICALTIATLAAACGIGAAAACCAAAAGCALTICAGAALAAATACTAACA 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27.4; DB 3; Length 582;
Pred. No. 23;
0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1118 B1-559-81-6856
Fax: 81-559-81-6855
Email: tshini@geneg.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                 /dl_xref="taxon:8090"
/clone="MF01SSA008A02"
/sex="mixture of female and male"
/issue_type="whole embryo"
/dev_stage="segmentation stage 20
/clone_lib="MF01SSA_CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Octaba Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                             organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total hq bases = 590
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Hd-rR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI953957.1 GI:16299057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 50.7%;
1 Similarity 69.8%;
37; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library
Unpublished (2001)
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Best Local Similarity
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/done lib="Hordeum vulgare green seedling EST library //lone lib="Hordeum vulgare green seedling EST library HVcDNA\(\text{D}\)014 (Blumeria infected)"
//note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2: Xhof; Morex (mla) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria graminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified con Albarary was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (COGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wingy Yu, Frisch, Henry, Simmons, Ostes, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or enemance analysis or preparation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                802 bp DNA linear GSS 12-AUG-20 clone LE HBa0169A20 3, genomic survey sequence.
DU032104.1 GI:72445405
GSS 5.
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Lycopersicon esculentum
                                  tissue_type="green seedling leaf"
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Tel: 607-255-6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2005)
Other GSSs: 13518
Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
Cornell University
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81.1%; Pred. No. 46;
tive 0; Mismatches
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Plate: 169 row: A column: 20
Seg primer: SP6
/clone="HVSMEm0015112f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence analysis see
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Best Local Similarity
Matches 36, Conserva
                                                                                                                                                           Query Match
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Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 83 Millian Basepairs of CDNA Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T31184 274 bp mRNA linear EST 06-SEP-1995 EST28439 Human Brain Homo sapiens cDNA 5' end similar to None, mRNA
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for clone availability, additional sequence and expression. '
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                     Length 802;
                                                                                                                                                                                                                                                 /lab host="E. col!"
/clone_lib="Tomato HindIII BAC Library"
/note="Vector: pBeloBAC11; Site_1: HindIII"
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                                                                                                                                                                                                                                                                                                                                                                                ch 49.3%; Score 26.6; DB 10; Length 1. Similarity 71.4%; Pred. No. 46; 35; Conservative 0; Mismatches 14; Indels
                                                                                                                              organism="Lycopersicon esculentum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
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                                                                                                                                                   /mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
/clone="LE_HBa0169A20"
                     High quality sequence start: 36
High quality sequence stop: 428.
Location/Qualifiers
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Class: BAC ends
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/done lib="Hordeum vulgare green seedling EST library /clone lib="Hordeum vulgare green seedling EST library HVCDNA0014 (Blumeria infected)"
//note="Vector: pBlueeript SK(-); Site_1: ECORI; Site_2: XhoI; Morex (mla) plants were greenhouse grown in the R wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria graminis f: sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TV Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVSMEm0015E24f Hordeum vulgare green seedling EST 19-OCT-200: HVCDMA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA clone HVSMEm0015E24f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta;
Booideae; Triticeae; Hordeum.
1 (bases I to 771)
Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Oates, R. and Main, D.
Bovelopment of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                        41
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                                                                                                                                                                                                                                                                                                                                                                        93 ATTTATTTCAATTAACTAAAATTCCAAAAACTTATCACNAAAAATGAGACAAC
                                                                                                                                                                                                                                                                                                                         2 ATCTGATTGATTGAACGAAAAACGCGAAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                         Length 274;
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/lab_host="TJC121"
                                                                                                                                                                                            DB 8;
/db_xref="ATCC (inhost):101229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
                                                                                                                                                                                         Score 26.4; DI
Pred. No. 53;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
Total hq bases = 486
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence start: 16
High quality sequence stop: 619.
Location/Qualifiers
                          /db_xref="taxon:9606"
/clone lib="Human Brain"
/note="Organ: brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEm0015E24f"
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/cultivar="Morex"
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                                                                                                                                                                                     48.9%;
ilarity 67.9%;
Conservative 0
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Unpublished (2001)
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ORIGIN

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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

E 1 (bases 1 to 215)
S Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Oates,R. and Main,D.
Devalopment of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
CDNA library
L Unpublished (2001)
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                                                                                                                                                                                                     sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored BST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
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/clone lib-Hordeum vulgare green seedling EST library
HVcDNA0014 (Blumeria infected)
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Morex (mla) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 48.9%; Score 26.4; DB 3; Length 771; 1 Similarity 75.0%; Pred. No. 54; 33; Conservative 0; Mismatches 11; Indels 0
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100 Jordan Hall, Clemson, SC 29634, USA
Trel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
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/clone="HVSMEm0015K12f"
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/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 33; Conserv
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KEYWORDS
SOURCE
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green seedlings were infected with isolate 5874 of Blumeria graminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give phluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Prisch, Aktins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see thtp://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wiss R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
I (bases I to 771)
Wing, R., Close, T.J., Kleinhofe, A., Wise, R., Chin, A., Begum, D.,
Prisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (Compatible) seedling
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/mol_type="mRNA"
/cultivar="Morex"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Contact: Wing RA
Clemson University Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 26.2; 1
Pred. No. 62;
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Total hd bases = 471
Seq primer: ATTAACCTAAAGGG
High quality sequence start: 25
High quality sequence stop: 736.
Location/Qualifiers
e 1...771
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ilarity 79.5%;
Conservative (
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Best Local Simil
Matches 31; (
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BH821089 510 bp DNA linear GSS 20-MAY-2002 BACPP15-D03.y Pristionchus pacificus BAC ends Pristionchus pacificus genomic, genomic survey sequence.
                                                                                                                Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MEI-0032P-A101 row: 3 column: F.
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
Brasil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Srintvasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A., Jesse, T., Millare, J., de Both, M., Schuster, S.C. and Sommer, R.J. A BAC-based genetic linkage map of the nematode Pristionchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 510)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ATCTGATTGATTGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Length 510;
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/mol_type="genomic DNA"
/strain="var, California"
                                                                                                                                                                                                                                                                                                                                                                    /organism="Schistosoma mansoni"
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/db_xref="taxon:6183"
/clone="ME1-0032P-A101-F03.B"
/sex="mixed pool"
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/lab_host="Mus musculus"
/clone_lib="ME1-0032"
/note="Vector: pGEM T-easy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
48.1%; Score 26; DB
Best Local Similarity 70.0%; Pred. No. 74;
Matches 35; Conservative 0; Mismatches
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Pred. No. 75;
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Class: BAC ends.
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Pristionchus pacificus
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Contact: Sommer RJ
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                                                                                                                                    /clone libe-Hordeum vulgare green seedling EST library /clone libe-Hordeum vulgare green seedling EST library HVCDNA0014 (Blumeria infected) "
/note="Vector: pBluescript SK(-) Site_1: ECORI; Site_2: XhOI; Morex (mla) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammins f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture one primary unamplified CDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Palmer, Arkins and Wing). Plasmid DNA preparations. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD113955 384 bp mRNA linear EST 14-SEP-2003 ME1-0032P-A101-F03-U.B ME1-0032 Schistosoma mansoni cDNA clone ME1-0032P-A101-F03.B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashron,P.D., Bonaldo,M.F., Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L., Nascimento,A.L.T.C., Ohlweiler,R.R., Ris,E.M., Ribeiro,M.A., Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T., Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  franscriptome analysis of the acoelomate human parasite Schistosoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored BST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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Strigeidida; Schistosomatoidea; Schistosoma.
1 (bases 1 to 384)
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                                                                                         'tissue_type="green seedling leaf"
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Departamento de Bioquimica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match
Local Similarity 79.5%; Pred. No. 64; les 31; Conservative 0; Mismatches
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                                  /db_xref="taxon:112509"
/clone="HVSMEm0015G22f"
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 1 GATCTGATTGATTGAACGAAAAACGCGAAAAGCGTTTCACGATAAATGCGA 50

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 253 GATCATATTGATTAATGAAAATCGGGGAAGCGGATATTTAGAAATGAGA 302

Search completed: January 18, 2006, 11:40:45 Job time : 232.555 secs AF519766 Cloning v AY428809 Cloning v AY781400 Synthetic U81140 Shigella AF25777 Shigella AY781404 Synthetic AY781404 Synthetic AY289598 Cloning v AF060240 Mobile an AY222812 Cloning v AY222812 Cloning v AY222812 Cloning v AF05289 Cloning v AF121784 Expression AF052036 Expression AF0569 Reporter AF0569 Reporter AF05696 Reporter AF0569 Reporter AF0569 Reporter AF0569 Reporter AF0569 Cloning v AF0569 Reporter AF0569 Cloning v AF0569 Reporter AF0569 Cloning v AF0569 Cloning v AF0569 Cloning v AF0569 Cloning v AF0569 Cloning vector AF30518 Expressio L08855 pBR325 Cloning vector AF30503 PBR325 Cloning ve

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3053 AAAAAGGATCATATCGTCAATTATTACCTCCACGGGAGAGCCTGAGCAAACTGGCCTCA
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Pred. No. 6.6e-309;
0; Mismatches 18; Indels 0;
                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

1 (bases 1 to 3400)

Carstens,C.-P.
Method for transfer of DNA segments
Patent: US 6696278-A 1 24-FEB-2004;
Stratagene; La Jolla, CA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             3400 bp
Sequence 1 from patent US 6696278.
AR477289
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AF405696
AF405697
AY230218
SYNPBR328V
SYNPBR325V
D88215
SYN261CAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
/wol_type="genomic DNA"
        AY428809
AY781400
SFU81140
AF326777
AY781404
AY289598
AF060240
AY22812
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AB001326
AB052891
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AX55422 Sequence
AX642149 Sequence
AX54420 Sequence
U46018 Cloning vec
CS119871 Sequence
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AF155422 Cloding v
M37690 Acinetobact
M62822 Abaumannii
AY608912 Escherich
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AY303236 Shuttle v
AY22353 Klebsiell
AP000342 Plasmid R
AJ851089 Unculture
AL513383 Salmonell
                                                            2006, 18:06:53; Search time 6461.19 Seconds (without alignments) 11032.288 Million cell updates/sec
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                                                                                                                   1 gatctgattgattgaacgaa......ttcgttcaatcaatcagatc 1254
        5.1.6
Compugen Ltd.
                                                                                                                                                                5883141 segs, 28421725653 residues
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        version 5
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        GenCore (c) 1993
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seq length: 200000000
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PAT 14-MAY-2004

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AR072535 Sequence

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111442 1114422 11113522 11113522 11113522 1112396 1112396 1112396 1112396 1112396

Result No.

2814

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                REFERENCE
AUTHORS
TITLE
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                                   TGTTGTAATTCATTAAGCATTCTGCGGACATGGAAGCCATCACAACGGCATGATGAACC
                                                                                                            ACGGGGCGAAGAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
                                                                                                                     CAGGGATTGGCTGAGACGAAAACATATTCTCAATAAACCCTTTAGGGAAATAGGCCAGG
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PAT 27-NOV-2002

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6122 bp WO0246436.

AX554413 Sequence 1 from Patent 1 AX554413 AX554413.1 GI:25898196

RESULT 2
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                               Bowdish,K.S., Barbas-Frederickson,S., Wild,M.
Novel plasmid vectors
Patent: WO 0246436-A 1 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Pred. No. 1.1e-307;
0; Mismatches 2;
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="t-axon:32630"
/note="plasmid"
other sequences; artificial sequences
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6125 bp
Sequence 8 from Patent W00246436.
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Bowdish, K.S., Barbaberere
and Mcwhirter, J.
Engineered plasmids and their use for in
Patent: WO 0246435-A 1 13-JUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers
                                                                               1. .6122
| Organism="synthetic construct"
|mol_type="unassigned DNA"
|db_xref="taxon:32630"
                                                                                                                                                                Score 1142.8; DB (Pred. No. 1.1e-307.0); Mismatches 2.
                                                                                                                             'note="vector"
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Best Local Similarity 99.8%;
Matches 1144; Conservative (
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Patent: WO 0244316-A B 13-UUN-2002;
ALEXION PHARMACEUTICALS, INC. (US)
Location/Qualifiers .; 3 1.1e-307; /organism="synthetic construct" |mol_type="unassigned DNA" |bxref="taxon:32630" |note="plasmid" DB DNA other sequences; artificial sequences. Score 1142.8; Pred. No. 1.1e-0; Mismatches

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Submitted (16-JAN-1996) Sam Marsh, Marketing Analysis, 11011 North Torrey Pines Road, La Jolla, CA 92037, USA Location/Qualifiers
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                                                                      Cam"
                                                                    PCRSCRIPT
                                                                                                                                                         DB 11;
                                                                                                                                                       90.5%; Score 1135.2; DB 11
98.4%; Pred. No. 1.5e-305;
tive 0; Mismatches 18;

    .3399
    /organism="Cloning vector
/mol_type="genomic DNA"
    /db_xref="taxon:45534"

                                                                                                                                                                         Best Local Similarity 98.4
Matches 1157; Conservative
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SYN 27-0CT-1999

linear

3399 bp DNA linea Cloning vector pCRSCRIPT Cam, complete sequence. U46018

CVU46018/c LOCUS DEFINITION

Cloning vector pCRSCRIPT Cam Cloning vector pCRSCRIPT Cam other sequences; artificial sequences; vectors.

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

Marsh, S. Direct Submission

REFERENCE AUTHORS TITLE

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1 (bases 1 to 1808)

Zhang, C., Kitsberg, D., Chy, H., Zhou, Q. and Morrison, J.R.
Transposon-mediated generation of targeting vectors for the
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Patent: WO 2005056782-A 133 23-JUN-2005;
GENENCOR INTERNATIONAL, INC. (US); THE PROCTER & GAMBLE COMPANY
(US)
                                                      TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACC
               GIGGTATATCCAGIGATTTTTTTTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGAC
                                                                                                                   ACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA
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Pred. No. 1.5e-305;
0; Mismatches 18; Indels
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1. .4100
Acgainsm="synthetic construct"
//nol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="pAH502R plasmid"
                                                                                                                                                                                                                                                                                                                                  Sequence 133 from Patent WO2005056782. CS119871. GI:70667769
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synthetic construct
other sequences; artificial sequences.
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/organism="Cloning vector pTG8"
/mol_type="genomic DNA"
/db_xref="taxon:119062"
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/transl_table=11
/product="lac2"
/protein_id="AAF61634.1"
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SSLWSEYHDDPRQFLHTYSQDVACYGBNLAYFPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNBLQQYGDBWQGG
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production of gene knockouts (er) Nucleic Acids Res. 33 (3), E24 (2005) In press
                                                                                                                                                                                                               'transposon="mini-Mu transposon TnCR1"
                                                                                         Pty Ltd,
                                                                                                                                                      construct"
                                                  Zhang,C.
Direct Submission
Submitted (14-OCT-2004) CopyRat Pty I
Clayton, Victoria 3168, Australia
Location/Qualifiers
                                                                                                                                                                                                                                           /codon_start=1
/trans1_table=11
/product="chloramphenicol
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/mol type="other DNA"
/db_xref="taxon:32630"
1. .1808
                                             (bases 1 to 1808)
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Yang, Y. and Spector, A.
Direct Submission
Submitted (21-MAY-1999) Institute of Molecular Biology, University of Hong Kong, 8 Sassoon, Pokfulam, Hong Kong
Location/Qualifiers
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ACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAATCGTCGTGGTA
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(bases 1 to 3417)

Yang, Y. and Spector, A.

Improved cloning vectors for transgene construction of the sequence of the sequen
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Draft entry and computer-readable sequence for [Unpublished (1990)]
Kindly submitted
by L.M.Steyn, 10-AUG-1990.
Univ of Cape Town
Dept Med Microbiol
Med Sch
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( (bases 1 to 1851)
Elisha, B.G. and Steyn, L.M.
Identification of an Acinetobacter baumannii gene region with
                                                                                                                                                                                                                                           2839 GTGGTATATCCAGTGATTTTTTTTTTTTAGCTTCCTTAGCTCCTGAAAATCTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
                                                                                                                                                                                                                                                                                                                                           2899 AACTCAAAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2719 TTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACAT
                                                                                                     TGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
                                                                                                                                                                                                          GTGGTATATCCAGTGATTTTTTTTTCTCCATTTTTAGCTTCCTTAGCTCCTGAAAATCTCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Original source text: Acinetobacter calcoaceticus anitratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence and organizational similarity to Tn2670 lbsmid 25 (2), 96-104 (1991)
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/gene="CAT"
/codon start=1
/transl_table=11
/protein id="RAA62571.1"
/db_xref="G1:141789"
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/db_xref="taxon:471"
/clone="pGSH201"
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Cape Town 7925 South Africa.
Location/Qualifiers
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/isolate="SAK"
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M37690.1 GT:141788
CAT gene; Tn2670-like transp
Acinetobacter calcoaceticus
Acinetobacter calcoaceticus
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SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
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                                                                                                                   Gaps
                                                                                          Length 1851;
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                                                                                        Score 1129.6; DB 1;
Pred. No. 5.4e-304;
0; Mismatches 14;
                                                                                        90.1%;
98.8%;
                                                                                                      Best Local Similarity 98.8
Matches 1138; Conservative
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/translation="withings of the control of the contro 1129 BCT 24-APR-1993 gene, complete 1274 ö 1214 1154 374 314 254 194 109 169 229 GTGGTATATCCAGTGATTTTTTTTTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGAT AACTCAAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTT ACGIGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCCGGTATCAACA Gammaproteobacteria; Pseudomonadales; ATAAATGATCATATCGTCAATTATTACCCCCCAGGGGAGGCCTGAGCAAACTGGCCTCA 1213 ATAGACATAAGCGCTATTTAACGACCCTGCCCTGAACCGACGACGGGTCGAATTTGCT 1070 ACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA GGCATTTGAGAAGCACACGCTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGCA AAAACGGATCCTATCGTCAATTATTACCTCCACGGGGAGGCCTGAGCAAACTGGCCTCA GGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGCA ATAGACATAAGCGGCTATTTAACGACCCTGCCTGAACCGACGACGGGTCGAATTTGCT Gaps region with Score 1129.6; DB 1; Length 1874; Pred. No. 5.4e-304; 0; Mismatches 14; Indels 0; acetyltransferase" CACEAA 110ear 1874 bp DNA linear beammannii chloramphenicol acetyltransferase (cat) baumannii gene city to Tn2670 "iinamanii Bacteria; Proteobacteria; Gammaproteobacte Moraxellaceae; Acinetobacter. I (bases 1 to 1874) Elisha, B.G. and Steyn, L.M. Identification of an Acinetobacter baumanr sequence and organizational similarity to Plasmid (1991) In press Original source text: A.baumannii DNA. /codon start=1 /transl_table=11 /product="chloramphenicol ac/ /protein_id="AAA21891.1" /db_xref="G1:141745" 1. .1874 /organism="Acinetobacter ba /mol_type="genomic DNA" /db_xref="taxon:470" 405. .1064 M62822.1 GI:141744
choramphenicol acetyltransferase.
Acinetobacter baumannii
Acinetobacter baumannii

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                                                                                                                                                                                                                     Rakowski, S.A., Wild, J. and Filutowicz, M.
Direct Submission
Submitted (27-APR-2004) Bacteriology and Oncology, University of
Wisconsin - Madison, 420 Henry Mall - Room 151, Madison, WI 53706,
USA
                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="compared to plasmid pFL130; results in
phenylalanine to serine substitution; predicted to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431. .1348
/gene="pir"
/note="replication initiator (Rep) for R6K"
Escherichia coli plasmid pFL129, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="chloramphenicol resistance marker"
                                                                                                                                                   Wild, J., Czyz, A., Rakowski, S.A. and Filutowicz, M. Mobilizable gamma ori plasmid pFL129 sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uoue="contains 22 bp direct repeat"
/bound_moiety="Rep protein pi"
| 131. .1348
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/note="gamma origin of plasmid
1. .106
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complement(4180. .5454)
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107. .198
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1 (bases 1 to 6464)
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DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
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TITLE
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                                                                                                       TAAGGGCACCAATAACTGCCTTAAAAAATTACGCCCCGCCCTGCCACTATCGCAGTAC
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J. Bacteriol. 186 (8), 2393-2401 (2004)
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                                     TTTTCACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAATCGTCG
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Submitted (19-MXY-2003) Microbiology, University of Minnesota,
196, 420 Delawara Street S.E., Minneapolis, MN 55455, USA
Location/Qualifiers
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Shuttle vector pLEIItd+KR''deltaORF
other sequences; artificial sequences; vectors.
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GPRKGDD"
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/db_xref="G1:47717947"
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MSACFGFGWVAGPVLGGLMGGFSPHAPFFAAAALNGLNFLTGCFLLPESHKGBRRPFLR
ILAASFRWARGWTVAALMAUFFINGLVGQVPAALWVIFGEDRFHWDATTIGIS
LAAFGILHSLAQAMITGPVAALMAUFFINGLVGGVPRALWVIFGEDRFHWDATTIGIS
LAASGGIGMPALQAMITGPVAARLGERRALMCGMIADGTGYILLAFATRGWMAFPINVL
LAASGGIGMPALQAMITGPVAARLGGRRALMCGMIADGTGYILLAFATRGWMAFPINVL
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                                                                                                                                                                                                                                                                                                                                                                             'note="tetracycline resistance repressor protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                       protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1129.6; DB 1;
Pred. No. 5.6e-304;
0; Mismatches 14;
                                     'note="tetracycline resistance
 .5454)
complement (4180.
/gene="tetA"
                                                      /codon_start=i
/transi_table=11
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                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                    5458. .6135
/gene="tetR"
                                                                                                                                                                                                                                                                                                                                        5458. .6135
/gene="tetR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.1%;
llarity 98.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 1138; Conser
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                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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SSLWSEYHDDFRQFLHIXSQDVACYGENIAYFPKGFIENMFFVSANPWVSFTSFDLNV
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                                                                                                                                                                                   /translation="mmfnkidldnwkrkelfnhylnocytfsitteidisvlyrniko
bgykfypafiflutrvinsntafrtgynsdgelgywdkleplytifdgvsktfsgiwt
pvkndfkefydlylsdvekyngsgklfpktpipenafslsiipwtsftgfnlninns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANMONFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                            /note="functions in gram negative bacteria; derived from
plasmid pACYC184 found in GenBank Accession Number X06403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
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                                                                                                                                                                                                                                                             NYLLPIITAGKFINKGNSIYLPLSLQVHHSVCDGYHAGLFMNSIQELSDRPNDWLL"
                 /note="functions in gram positive bacteria; derived from pC194 found in Genbank Accession Number V01277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10348 ATAAATGATCATATCGTCAATTATTACCTCCACGGGAGAGCCTGAGCAAACTGGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10888 ITTTCACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAAACTGCCGGAAATCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCATTTGAGAAGCACACGCTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10588 TAAGGGCACCAATAACTGCCTTAAAAAAATTACGCCCCGCCCTGCCACTCATCGCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10648 TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 GGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAAACCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10468 ATAGACATAAGCGGCTATTTAACGACCCTGCCTGAACCGACGACGGCCGGGTCGAATTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10528 TTCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAGGGCACCATAACTGCCTTAAAAAATTACGCCCCGCCCTGCCACTCATCGCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAATCGCCAGCGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            470 ACGGGGGCGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGGATTGGCTGAGACGAAAAACATATTCTCAATAAACCTTTAGGGAAATAGGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGGGTCGAATTTGCT
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0
                                                                                                                   acetyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1129.6; DB 11;
Pred. No. 5.7e-304;
0; Mismatches 14; In
                                                                                             /transl_table=11
/product="chloramphenicol
                                                                                                                                                                                                                                                                                   complement (10617. .11276)
                                                                                                                                         /protein_id="AAP73800.1"
/db_xref="GI:32185270"
                                                                    /codon_start=1/transl_table=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 1138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170
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/product=replication protein E"
/product=replication=10.00
/db_xxef="d1:32186268"
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FKSVKAARIISQNIREYFGKSLPVDLTCNHFGIARIPRTNVFFFDPNYFFSKEWQD
FKSVKAARIISQNIREYFGKSLPVDLTCNHFGIARIPRTNVFFFDPNYRYSFFREWQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2594. .2605
/note="derived from T4 phage thymidylate synthase found in
GenBank Accession Number M12742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
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/dprotein_id="AAP73802.1"
/db_xref="G186272"
/translation="MAKMRISPELKKLIBKYRCVKDTEGMSPAKVYKIVGEN$NLYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase found in exon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTDSRYKGTTYDVEREKDMMLMLEGKLPVPKVLHFERHDGWSNLLMSEADGYLCSEEY
BDGGSPEKLITELYAECTRIFHSTDISDPTYNLDNDLADVLCSNWE
EDTPFKDPRELYDFKTEKPERELVFSHGDIGDSNIFWYDGKVGGFTDLGRSGRADKW
YDIAFCVRSIREDIGEEGYVELFFDLLGIKPDWEKIKYYILLDELF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSFKQTDNKGFTRSSLTVLSGTEGKKQVDEPWFNLLLHETKFSGEKGLIGRNNVMFTL
SLAYFSSGYSIETCEYNMFERNRLDQPLEBKEVIKUVRSAYSENYQGANREYTILC
KAWVSDLTSKDLFVRQGWFFKKKRSERQRYHLSEWKEDLMAYISEKSDVYKPYLVT
TKKEIRENYGIPERTLDKLLKVLKANGEIFFKUKPGRNGGIQLASVKSLLLSIIKVKK
EEKESYIKALTNSFDLEHTFIQETLNKLARRARENTDTQLDLFSYDTG"
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DKYFSSEGEDY1YKLIENNKI1YSISGKKLTYKGKKSFSKHAILKQLNEKANQVN"
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amiakqrktlyvcfhchrhvihkhk"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3255. .4049
//note=-13./5'aminoglycoside phosphotransferase; kanamycin
resistance; from enterococcal plasmid pJHl found in
GenBank Accession Number V01547"
                                                                                                                                                                                           APHIII and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (5166, .6656)
/note="pIL253 replication in gram positive bacteria;
derived from GenBank Accession Number AF041239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6699. .6998)
/note="pIL253 replication in gram positive bacteria;
derived from GenBank Accession Number AF041239"
                   /organism="Shuttle vector pLEIItd+KR''deltaORF"
/wol_type="genomic DNA"
/db_xref="taxon:234876"
                                                                                                                                                           1803. .4225
/note="Ll.ltrBdeltaORF group II intron with
tddelta(1-3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2999. .3010
/note="derived from T4 phage thymidylate
GenBank Accession Number M12742; partial
                                                                                                                                                                                                                                    2376. .2585
/note=maturase with internal deletion"
/codon start=1
/transI_table=11
/product="ltrafdeltaORF"
/protein id="AAP73797.1"
/db_xref="G1:32185267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606. .2998
note="tddelta(1-3) group I intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۵
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/protein_id="AAP73799.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4226. .4316
/note="ltrBE2; partial exon"
                                                                                           .623. .1802
'note="ltrBE1; partial exon"
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transl_table=11
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/ trānslation="MKPTMAILERISKNSQENIDEVFTRLYRYLLRPDIYYVAYQNLY
SNKGASTKGTLDDTADGFSERKIKKIIQSLKOGTYYPOPVRRMYIAKKNSKKNRPLGI
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IKGCPDNIDHYTLLIGLINLKIKDMRKNSQLIYKFLKAGYLENWQYHKTYSGTPQGGILS
PLLANIYLHELDKFVLQLKWKFDRESPERITPEYRELHNEIKRISHRLKKLEGEEKAK
VLLEYQEKRKRLPTLPCTSQTNKVLKYVRYADDFIISVKGSKEDCQMIKEQLKLFIHN
                                                                                                                                                                                                                                                                                                                                                KLKMELSEEKTLITHSSQPARFLGYDIRVRRSGTIKRSGKVKKRTLNGSVELLIPLQD
KROQFIPKKALALQKKOSSWPPVHRKYLIRSTDEIITIYNSELRGINYYGLASNRN
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BCKSPYQFTDEISQAPVLYGYARNTLENRLKAKCCELCGTSDENTSYEIHHVNKVKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTDSRYKGTTYDVEREKDMMLWLEGKLPVPRVLHFERHDGWSNLLMSEADGVLCSEEY
BEDGSPEKITIELYAECIRLFHSIDISDCPYTWSLDSRLAELDYLLMNDLADVDCENWE
EDTPFWDPRELYDFLKTERFEELVESHGDLGDSNIFVKDGRVGGFIDLGRSGRADKW
YDIAPCVRSTREDIGERGYVELFFDLLGIKDWEKIKYYILLDELF"
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WSFKQTDNKGFTRSSLTVLSGTEGKKQVDEPWFNLLLHETKESGEKGLIGRNNVMFTL
SLAYFSGSGSIETCEYNMFERNRLDOPLEEKEVIKIVRSAYSENYGGANREYITLC
KAWYSSDLTSKDLFVRQGWFFKKKRSFROWNLSEWKEDLWAYISEKSDVYKPYLVY
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EEKESYIKALTNSFDLEHTFIQETLNKLARERPKTDTQLDLFSYDTG"
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/note="3",5",aminoglycoside phosphotransferase; kanamycin
rote="stance; from enterococcal plasmid pJH1 of GenBank
Accession Number V01547"
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/note="derived from GenBank Accession Number AF041239"
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/note="derived from T4 phage thymidylate synthase of
GenBank Accession Number M12742"
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/note="derived from T4 phage thymidylate synthase of
GenBank Accession Number M12742; partial exon"
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/note="pIL253 replication in gram positive bacteria;
derived from GenBank Accession Number AF041239"
                    ţ
                      and
         /note="L1.ltrB group II intron with APHIII delta(1-3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4196. .4588
/note="td delta(1-3) group I intron"
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/transT_table=:
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Submitted (16-MAY-2003) Microbiology, University of Minnesota, MMC
196, 420 Delaware Street S.E., Minneapolis, MN 55455, USA
Location/Qualifiers
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Staddon, J.H., Bryan, E.M., Manias, D.A. and Dunny, G.M.
Conserved Target for Group II Intron Insertion in Relaxase Genes
Conjugative Elements of Gram-Positive Bacteria
                                                                                                                                                                                                                                                     TTCTTTACGGTCTTTAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACAT
10948 TGGTATTCACTCCAGAGGGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAA
                                        GGGTGAACACTATCCCCATATCACCAGCTCACCGTCTTTCATTGCCATACGTAATTCCGGA
                                                               TGAGCATTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAAACTTGTGCTTATTT
                                                                                                                                                   11068 TGAGCATTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGGATAAAACTTGTGCTTATTT
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Shuttle vector pLEIItd+KR',
other sequences; artificial sequences; vectors.
1 (bases 1 to 13515)
Cousineau, B., Lawrence,S., Smith,D. and Belfort,M.
Retrotransposition of a bacterial group II intron
Nature 404 (6781), 1018-1021 (2000)
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/organism="Shuttle vector pLEIItd+KR'"

/moltype="genomic DNA"

/moltype="taxon:233895"

1623. .1802

/note="ltrBE1; partial exon"
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Shuttle vector pLEIItd+KR'', complete sequence.
AY303236
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Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
1 (bases 4901 to 22900)
Partridge, S.R. and Hall, R.M.
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Partridge,S.R. and Hall,R.M.
The IS1111 family members IS4321 and IS5075 have subterminal inverted repeats and target the terminal inverted repeats of Tn21
                                                                                                                                                                                                                                                                                                                    TGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
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                                                            GGGTGAACACTATCCCATATCACCAGCTCACCCGTCTTTCATTGCCATACGTAATTCCGGA
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J. Bacteriol. 185 (21), 6371-6384 (2003)
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J. Bacteriol. 185 (21), 6371-6384 (2003)
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AUTHORS
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                                                                                                                                                                                                                                                                                                              /codon start=1
/trans_trable=11
/trans_trable=11
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/product="chlo=mphenicol acetyltransferase"
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SSLWAEEVHDDFRQFLHIYSQDVACYGBNLAYFPKGFIENMFPVSANPAVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNBLQQXCDEWQGG
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                                                                                                                                                                             /trānslation="MNFNKIDLDNWKRKEIFNHYLNQQTTFSITTEIDISVLYRNIKQ
EGYKFYPAFIFLVTRVINSNTAFRTGYNSDGELGYWDKLEPLYTIFDGVSKTFSGIWT
PVKNDFKEFYDLYLSDVEKYNGSGKLFPKTPIPENAFSLSIIPWTSFTGFNLNINNNS
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                                                                                                                                                                                                                                   NYLLPIITAGKFINKGNSIYLPLSLQVHHSVCDGYHAGLFMNSIQELSDRPNDWLL"
complement(12207. .12866)
/note="functions in gram negative bacteria; derived from
plasmid pACYC184 of GenBank Accession Number X06403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650 TGGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAA 709
                        9929. .10579
/note="functions in gram positive bacteria; derived from
pC194 of GenBank Accession Number V01277"
      )KYFSSEGEDYIYKLIENNKIIYSISGKKLTYKGKKSFSKHAILKQLNEKANQVN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAACGGATCCTATCGTCAATTATTACCTCCACGGGGAGAGCCTGAGCAAACTGGCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12298 TGAATCGCCAGCGCATCAGCACCTTGTCGCCTTGCCGTATAATATTTGCCCATGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGGGGGGAAGAGTIGICCATATIGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGGGGGGGGAAGAGTGGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICGAATITCIGCCATICATCGCTIATIATCACTIATICAGGCGTAGCAACCAGGCGTT
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Pred. No. 5.7e-304;
0; Mismatches 14; Indels 0; Gi
                                                                              /codon_start=1
/transl_table=11
product="chloramphenicol acetyltransferase"
protein_id="AAP70041.1"
db_xref="GI:32140768"
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98.8%;
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Best Local Similarity 98.8
Matches 1138; Conservative
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/protein_id="AAMS913.2"

/db_xref="G1:28558820"

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LERLLAFWREGGTVVHSMPRLARNLDDLRRIVGGTTQRGVRNEFVKEGLKFTGEDSP

MANLALSVMGARAEREALIRERQREGIVLAKQRGAYRGRKKSLNSEQIAELKRRVAA

GDQKTLVARDFGISRETLYQYLRED"
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EIGRPRPSRRLPVVLTPDEVVRILGFLEGEHRLFAQLLYGTGMRISEGLQLRVKDLDF
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HTLRHSFATALLRSGYDIRTVQDLLGHSDVSTTMIYTHVLKVGGAGVRSPLDALPPLT
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/notes=attI1; integron-associated recombination site
recognised by IntI1"
6472. .7062
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/note="5'-CS; 5'-conserved segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transposon="class I integron In34"
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/transl_table=11
/product="IntIl integrase"
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/note="aadB gene cassette"
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/note="left-hand inverted
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complement(5322. 6335)
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/db_xref="GI:24527229"
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/note="Tn1696 resIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5072. .5105
/note="Tn1696 resII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAKVGAGKFRPLRPLPPA"
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/transl_table=11
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| Da xref="G1:2858821"
| translation="WENIALIGIDLGRUSFHIHCQDRRGKAVYRKKFTRPKLIEFLAT
| translation="WENIALIGIDLGRUSFHIHCQDRRGKAVYRKKFTRPKLIEFLAT
CPATTIAMEACGGSHFMARKLEELGHFPKLISPQFVRPFVKSNKNDFVDAEAICEAAS
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LITALEBDNSTPLYLSQULLKQQHYHYTVDQTDCDLSSQLKRKLDBBEGORKLBEBE TOCY
GTLTARTISTEIGDSKYASSRPRAATGLVPRQYSTGGRYTLLGISKRGNKKTRTLL
VQCARVPIQKLBHQSGKLADWVRDLLCRKSNFVVTCALANKLARIAMALTARQQTYVA
                                                                                                                                                                                                                                                                                             Submitted (17-JUN 2002) CSIRO Molecular Science, PO Box 184, North Ryde, NSW 1670, Australia (17-JUN 2002) CSIRO Molecular Science, PO Box 184, North Ryde, NSW 1670, Australia (25-FEB-2003) CSIRO Molecular Science, PO Box 184, North Ryde, NSW 1670, Australia (25-FEB-2003) CSIRO Molecular Science, PO Box 184, North Ryde, NSW 1670, Australia (25-FEB-2003) CSIRO Molecular Science, PO Box 184, North Ryde, NSW 1670, Australia (25-FEB-2003) CSIRO Molecular Science, PO Box 184, North Ryde, NSW 1670, Australia (25-FEB-2003) CSIRO Molecular Science, PO Box 184, North Partridge, S. R. and Hall, R. M.
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/organism="Klebsiella pneumoniae"

/organism="Flebsiella pneumoniae"

/organism="Repeated by the properties of the properties o
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Submitted (12-MAR-2003) CSIRO Molecular Science, PO Box 184, North
Ryde, NSW 1670, Australia
8 (bases 1 to 45325)
Partridge,S.R. and Hall,R.M.
Direct Submission
Partridge, S.R. and Hall, R.M.
Complex multiple antibiotic and mercury resistance region derived
from the r-det of NR1 (R100)
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                                                                                                                   Antimicrob. Agents Chemother. 48 (11), 4250-4255 (2004)
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/product="TnpA transposase"
/protein_id="AAO46047.1"
/db_xref="G1:28558822"
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/rpt_type=inverted
complement(1484, .4456)
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note="IRr of IS4321"
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Partridge, S.R. and Hall, R.M.
Direct Submission
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IDLTFPGERRGELEAIVEMLGGRVWEELDYGFLAEIGDELLDCEPAWWADEAYEIAEA
PQGSCPEAABGVIAGRPVRCNSWEAIIWDYFYYADEVPPVDWPTKHIESYRLACTSLG
AEKVEVLRAAFRSRYAA"
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                                                                                                                                                                                                                                                                   7063. .8375
/note="3'-CS1; first copy of 3'-conserved segment; bases 1-1313 of standard 3'-CS"
7063. .7452
join(7009. .7062,6472. .6477)
/note="aadB 59-be; 59-base element; IntI-type integrase
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product="aminoglycoside
AD(2'')"
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/db_xref="G1:24527230"
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/gene="aadB"
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Compugen Ltd.
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1 gatctgattgattgaacgaa......ttcgttcaatcaatcagatc 1254 9993994 Total number of hits satisfying chosen parameters: 4996997 seqs, 3332346308 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence: Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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No.	Score	Match	Match Length DB	DB	ID	Description
-	1254	100.0	1254	101	ACF58169	Acf58169 Modified
ر د	1147.2	91.5	3400	7	ADL18593	Adl18593 Plasmid p
3	1142.8	91.1	6122	9	ABN84078	Abn84078 Plasmid p
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c 11	1116	89.0	9808	14	ADZ66224	Adz66224 Construct
c 12	1116	89.0	9808	14	AEB80052	Aeb80052 Vector pA
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14	1114.4	88.9	5838	7	AAV28398	Aav28398 Plasmid p
15	1114.4	88.9	5838	7	AAZ06434	Aaz06434 Plasmid p
16	1114.4	88.9	5838	7	AAZ22882	Aaz22882 Plasmid p
c 17	1114.4	88.9	7814	9	ABK87209	Abk87209 Synthetic
18	1114.2	88.9	3064	14	ADV09403	Adv09403 Plasmid p
19	1106.6	88.2	5300	14	ADY91370	Adv91370 E. coli

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88.2	85.7	85.4	83.9	83.9	83.9	83.9	79.6	78.4	78.4	78.4	78.4	78.4	78.4	78.4	78.4	9.9/	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0
1105.6	1074.8	1070.4	1052.4	1052.4	1052.4	1052.4	998.2	982.6	982.6	982.6	982.6	982.6	982.6	982.6	982.6	096	952.8	952.8	952.8	952.8	952.8	952.8	952.8	952.8	952.8
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ALIGNMENTS

Transposon; genetic engineering; transposase; Cat-Mu; ds. Modified Cat-Mu(Stop) -transposon. BP. ACF58169 standard; DNA; 1254 14-APR-2003; 2003WO-FI000285. 18-APR-2002; 2002FI-00000746. (first entry) Savilahti H, Tieaho V; (FINN-) FINNZYMES OY. WPI; 2003-845329/78. Bacteriophage mu. WO2003087370-A1. 15-JAN-2004 23-OCT-2003 Synthetic ACF58169; RESULT 1 ACF58169

New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by a transposase useful for producing deletion derivatives of polypeptide. Claim 6; Page 30; Opp; English.

The invention relates to a transposon nucleic acid comprising a genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of a

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transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence recognized by a transposase, and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a modified Cat-Mu(Stop)-transposon
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100.0%; Score 1254;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1254; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene transfer; product vector; purification; detection; plasmid; pBC SK+;
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CTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACGGTGGTATATCC
                                                                                                      AGTGATTTTTTTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGACAACTCCAAAAAA
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ADL18593/c
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selectable marker, where the gene encoding the negative selectable marker is interposed between the double-stranded origin of replication of a colling circle replication and the site-specific recognition site, where one or both of the vectors have no second site-specific recombinates as it e-specific recombinates as it e-specific recombination site, (2) a product vector comprising a gene, a double-stranded origin of replication of a rolling circle replication and a nucleic aid sequence encoding a second selectable replication and a nucleic aid sequence encoding a second selectable creplication and a nucleic aid sequence encoding a second selectable creplication of replication and the double-stranded origin of replication of a rolling circle replicon and the site-specific recombination site, and (3) a kit for the transfer of gene to crempination recognition site, and (3) a kit for the transfer of gene to a product vector comprising (1) and packaging materials. The method is useful in expressing mammalian cell and bacterial hosts, purification of the native protein by employing specialised purification tags and detection of interaction with other proteins. The present sequence represents the nucleotide sequence of plasmid pBC SK+, which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.5%; Score 1147.2; Best Local Similarity 98.5%; Pred. No. 0; Matches 1158; Conservative 0; Mismatches
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                                                        2273 TTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACAT
                                                                                                    2213 TGAGCAACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
                                                                                                                                                    2153 GTGGTATATCCAGTGATTTTTTTTTCTCCATTATAGCTTCCTTAGCTCCTGAAAATCTCGAC
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                                                                                                                                                                                                                                                                                         2333 TGAGCATTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAAACTTGTGCTTATTT
                                                                                        TGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
                                                                                                                                     GTGGTATATCCAGTGATTTTTTTTTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGAC
                                                                                                                                                                                                                              1070 ACGIGCCGAICAACGICTCAITITCGCCAAAAGIIGGCCCAGGGCIICCCGGIAICAACA
                                                                                                                                                                                                                                                                           TTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACAT
                                                                                                                                                                                 1010 AACTCAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTT
                                                                                                                                                                                                       2093 AACTCAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTT
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/note= "the CDS does not include a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product= "Amp frag"
note= "the CDS does not include a stop (013. .1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/product= "Chloramphenicol transferase"
complement(2052. .2651)
                                                                                                                                                                                                                                                                                                                                               1913 GAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCT 1878
                                                                                                                                                                                                                                                                                                                          1190 GAAAAGGATCCGTTTTCGCATTTATCGTGAAACGCT 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pTL5-CAT; vector; antibody; gene;
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/note= "lac promoter"
3009. 3029
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/note= "lac rep s
3036. .3039
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/note= "ori"
2831. .3046
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/*tag= g
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/*tag= a
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ABN84078/c
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1941 AAAAAGGATCATATCGTCAATTATTACCTCCACGGGAGAGCCTGAGCAAACTGGCCTCA 1882

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The present sequence is that of plasmid pRLS-CAT, a derivative of pcbmb 3X which has been modified to contain chloramphenicol resistance. The invention relates to the engineering of plasmids, of which pRL-CAT is a preferred example, for in aitu production of genes. It was found that nucleic acids encoding a polypeptide can be directly incorporated into a plasmid by DNA polymerisation or by reverse transcription of a nucleic acid template. Preferably, nucleic acids encoding at least a portion of an antibody can be directly incorporated into the plasmid by reverse transcription of mRNA. The plasmids are engineered to contain 2 template annealing sequences (see ABN84079-80 and ABN84082-83), i.e. a downstream primer that anneals to a first portion of a nucleic acid template, e.g. mRNA encoding at least a portion of an antibody, an upstream collar restriction site located between the 2 template annealing sequences. A sequence that anneals to a second portion of the template, and at least restriction site located between the 2 template annealing sequences. A single stranded DNA plasmid vector is produced containing a nucleic acid encoding at least a portion of a polypeptide, e.g. a light chain and/or a plasmid below that we be transformed into a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises two template annealing upstream collar sequence and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wild M;
                                                                                                                                                                                                                                                                                                                                                                    Gene= "Gene III"
note= "the CDS does not include a start codon"
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                                                                                                                                                                note= "the CDS does not include a stop codon" 1365. .5147
                 *tag= h
note= "light chain variable region stuffer"
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does not include a
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                                                                                                                                                 product= "pelB leader"
                                                                                                                                                                                                                                                                                   product= "Linker-His
note= "the CDS does n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbas-Frederickson S,
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                                                951. .4269
*tag≈ i
note≈ "Kappa Cns"
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misc_feature
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Mcwhirter J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a plasmid with a nucleic acid sequence of 6122, or 5683 base pairs fully defined in the specification. The invention more specifically relates to novel vectors capable of replication and expression of foreign genetic information in bacteria, been designed to overcome certain drawbacks of the pcombix plasmid. These new vectors include pRL5, pRL5-CAT, pRL5 asc-CAT and pRL5 bsi-CAT. This polymucleotide sequence represents the plasmid pRL5-CAT nucleic acid
                                                                                                                                                                                                                                                                                                                                            acid
                                                                                                                                       Plasmid, vector; replication; expression; foreign genetic; bacteria; cyanobacterium; Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5 bsi-CAT; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid useful in cloning and expression of foreign genetic
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  ed. No. 0;
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                                           Sequence 6122 BP; 1447 A; 1571 C; 1641 G; 1463 T; 0 U; 0 Other;
                                                                                      Length 6122;
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                                                                                      Score 1142.8;
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                                                                                                            Pred. No. 0;
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  sequence of the invention
                                                                                                          Similarity 99.8
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                                                                                      802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "CH1, His6 tag, HA tag, and gene III amino acid
921 ACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid; vector; replication; expression; foreign genetic; bacteria; cyanobacterium; Bscherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT; pRL5-CAT; pRL5 bsi-CAT; gene; ds.
                                           foreign genetic
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1050. .3115
*tag= b
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1013. .1672
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                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pRL5
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terium; Escherichia coli; pComb3X plasmid; pRL5; pRL5 asc-CAT;
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                             ACGTGCCGATCAACGTCTCATTTTCGCCAAAGTTGGCCCAGGGCTTCCCGGTATCAACA
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                                                                                                                                                                                                                                                                                                                                          "CH1, His6 tag, HA tag, and gene III
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pRL5-CAT; pRL5 bsi-CAT; gene; ds
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replication and expression of foreign genetic information in bacteria, such as, for example, cyanobacterium and E. coli. The new vectors have been designed to overcome certain drawbacks of the pComb3X plasmid. These new vectors include pRL5, pRL5-CAT, pRL5 asc-CAT and pRL5 bsi-CAT. This polynucleotide sequence represents the plasmid pRL5 CAT-Asc nucleic acid sequence of the invention
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                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                          Sequence 6125 BP; 1447 A; 1573 C; 1644 G; 1461 T; 0 U; 0 Other;
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Pred. No. 0;
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99.8%;
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          GTGGTATATCCAGTGATTTTTTTTTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGAC
                                     AACTCAAAAAATACGCCCGGTAGTGATCTTATTTTCATTATGGTGAAAGTTGGAACCTCTT
                                                AACTCAAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAAGTTGGAACCTCTT
                                                                            ACGIGCCGATCAACGICTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCCGGTATCAACA
                                                                                       ACGTGCCGATCCACGTCTCATTTTCGCCAAAGTTGGCCCAGGGCTTCCCCGGTATCAACA
                                                                                                                  New isolated perhydrolase having preset perhydrolysis to hydrolysis ratio, useful in cleaning, bleaching and disinfecting applications
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Ramer SW;
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                                                                                                                                                                                                                                                                                                        perhydrolase; bleaching; paper; pulp; cosmetics; vector;
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Poulose AJ,
                                                                                                                                                                                                                                                                                       perhydrolase expression vector pAH502R
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GS, Oh H,
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AEA43207 standard; DNA; 4100 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMV ) GENENCOR INT INC. (PROC ) PROCTER & GAMBLE CO.
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Scheibel JJ, Weyler W,
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                                                                                                                                                                                                                                                                                       smegmatis
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Query Match

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The invention relates to an adapter-directed display system for displaying an exogenous polypeptide on the outer surface of a genetic package, comprising an expression vector with esquence that encodes exogenous polypeptide fused to a first adapter sequence, and a helper vector with outer-surface sequences encoding proteins fused to a second adapter, the polypeptide is produced in a host cell to cause displaying a cut polypeptide. Also included are a helper vector for displaying a polypeptide on the outer surface of a genetic package (comprising, outer-polypeptide on the outer surface of a genetic package, where at least one of the surface presenting sequences is fused in-frame to adapter, the adapter acting, when the polypeptide is produced in a capters in outer surface of a genetic package (comprising a coding sequence encoding the outer surface of a genetic package (comprising a coding sequence encoding the polypeptide fused in-frame to a first adapter, where the vector is devoid of outer-surface sequences encoding any functional outer-surface proteins cof the genetic package, and expression of the polypeptide on the outer surface of the genetic package is mediated through non-covalent pairwise surface of the genetic package is mediated through non-covalent pairwise
2734 ACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCCAGGGCTTCCCCGGTATCAACA 2675
                                                           Adapter-directed display system having expression vector with sequence encoding exogenous polypeptide and helper vector, for displaying exogenous polypeptide e.g., receptor ligand on outer surface of genetic
                                      ds, adapter-directed display system, phage display; outer surface protein; homodimerisation domain; heterodimerisation domain; antigen-binding unit; cell surface receptor ligand; cytosolic protein; secreted protein; HA tag; OmpA;
                                                                                                                    1190 GAAAAGGATCCGTTTTCGCATTTATCGTGAAACGCT 1225
                                                                                                                                                      2614 GAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCT 2579
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                                                                                                                                                                                                                                                        ADD14893 standard; DNA; 3817 BP
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(ZHON/) ZHONG P.
(WANG/) WANG X.
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c interaction between the first adapter and a second adapter, where the second adapter is fused to an outer surface protein), a kit comprising the obove vectors in suitable packaging, a host cell comprising the vectors approve that is fused to an outer surface of a genetic package using the adapter-directed display system, a genetic package using outer surface the fusion polypeptide, a selectable library comprising several genetic packages (at least on its outer surface the fusion polypeptide, a selectable library comprising several genetic packages (at least on selectable library comprising several genetic packages (at least on selectable library comprising several genetic packages (at least on selectable library comprising several genetic packages (at least on sepecific interaction between a test agent and an exogenous polypeptide or that is displaying the exogenous polypeptide that is prepared using the adapter-directed display system, contacting the genetic package (involving providing a genetic package). The outer-surface sequences encode bacterial outer-surface proteins chosen from Lapp-OmpA, TraT, Pal, Opt, Inp and AlDA-I. The first complex on the genetic package). The outer-surface sequences encode bacterial outer-surface proteins chosen from Lapp-OmpA, TraT, Pal, Opt, Inp and AlDA-I. The first complex on the outer surface of agenetic package in a suitable host cell. The selectable library to obtain at causing a polypeptide with desired property, which involves providing translated in a suitable host cell. The selectable library to obtain at least one genetic package that encodes the polypeptide with the desired property is binding specificity to an agent of interest. Screening the selectable library further involves becauting the center of special package that encodes the polypeptide with the desired property is binding specificity to an agent of contains the genetic package that encodes the polypeptide with the desired property is binding specificity to an agent of property. The polypeptide with the d 349 2834 AAAAAGGATCATATCGTCAATTATTACCTCCACGGGAGAGCCCTGAGCAAACTGGCCTCA TTCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT TAAGGGCACCATTAACTGCCTTAAAAAATTACGCCCCGGCCTGCCACTCATCGCAGTAC TAAGGGCACCAATAACTGCCTTAAAAATTACGCCCCGCCCTGCCACTCATCGCGTAC TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGAAGACC an Lpp-OmpA-GR2 fusion protein using GABAb receptor GR2 domain as the AAAACGGATCCTATCGTCAATTATTACCTCCACGGGGAGAGGCCTGAGCAAACTGGCCTCA GGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGCA 2774 GECATTIGAGAAGCACACGGICACACIGCTICCGGIAGICAATAAACCGGIAAACCAGCA ATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGACCGGGTCGAATTTGCT TTCGAATTTCTGCCATTCATCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT TGAATCGCCAGCGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAA TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACC Gaps Length 3817; ï Sequence 3817 BP; 948 A; 930 C; 948 G; 991 T; 0 U; 0 Other; 2; Indels protein as a DB 10; Score 1130.8; Pred. No. 0; Mismatches invention which can express an exogenous ö 90.2%; Matches 1143; Conservative Best Local Similarity adapter sequence. 110 170 230 2654 2594 350 2534 410 20 290 ઠે 셤 ઠે 셤 ò 셤 à 셤 ઠે g, δ 셤 ઠ

2474 TGAATCGCCAGCGCCATCAGCACCTTGTCGCCTTGCCGTATAATATTGCCCATGGTGAAA 2415

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Yamada

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Kajiura

Mori K,

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nishi M, Yasuda S Yamanishi CO LITD

T, Yama Hara T,

Tobimatsu Azuma M,

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material f

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The invention relates to a method for manufacturing 3-hydroxypropionaldehyde involving dehydrating glycerol with diol dehydratase and/or glycerol dehydratese and microbial cells comprising diol dehydratase reactivation factor and/or glycerol dehydratase reactivation factor and/or glycerol dehydratase reactivation factor along a method for manufacturing 1,3-propanediol, a method for manufacturing 3-hydroxypropionic acid and methods for manufacturing acrolein, acrylic acid and acrylic ester. The dehydration reaction of glycerol is performed under aerobic conditions using microbial cells. This sequence represents plasmid Pl5a DNA used in the method of the invention.
                                                                                                                                Manufacture of 3-hydroxy propionaldehyde useful as raw mater
manufacturing 1,3-propanediol, by dehydrating glycerol with
dehydratase and/or glycerol dehydratase and microbial cells.
                                                                                                                                                                                      Example 1; SEQ ID NO 2; 40pp; Japanese
            29-SEP-2003; 2003JP-00337663,
                                    (JAPC ) NIPPON SHOKUBAI
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Sequence 6607 BP; 1518 A; 1801 C; 1831 G; 1457 T; 0 U; 0 Other;
                       Length 6607;
                       DB 14;
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                        Score 1116;
Pred. No. 0;
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98.6%;
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Matches 1136; Conservative
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29-SEP-2004; 2004WO-JP014213

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16-JUN-2005

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Pharmaceutical; P15a;

WO2005030972-A1 Plasmid P15a

07-APR-2005

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                                                                              hydroxypropionaldehyde involving dehydrating glycerol with diol dehydratase and/or glycerol dehydratase and microbial cells comprising diol dehydratase reactivation factor and/or glycerol dehydratase reactivation factor and/or glycerol dehydratase reactivation factor. The invention also relates to a method for manufacturing 1,3-propanediol, a method for manufacturing 3-hydroxypropionic acid and methods for manufacturing acrolein, acrylic acid and acrylic ester. The dehydration reaction of glycerol is performed under aerobic conditions using microbial cells. This sequence represents plasmid Pl5a DNA used in the method of the invention.
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Pred. No. 0;
                                                            invention relates to a method
   4; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                 89.0%;
98.6%;
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Dubensky TW,

Bruckheimer E,

Kinch MS,

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TGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
                                                                                                                                                                       TGAGCAACTGACTGAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recessive dystrophic epidermolysis bullosa; rheumatoid arthritis; ankylosing spondylitis; systemic lupus; psoriatic arthropathy; Reiters' syndrome; Sjogrens' syndrome; endometriosis; preeclampsia;
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24-DEC-2003; 2003US-053266F
26-MAR-2004; 2004US-0556531P.
01-OCT-2004; 2004US-0615470P.
07-OCT-2004; 2004US-0617544P.
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(CERU-) CERUS CORP.
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This sequence represents the expression cassette construct pAM401-MCS.
This sequence was used in the scope of the invention for the expression of EbpA2 is a 130 kD receptor tyrosine kinase that is expressed at adherent sequence was used in the scope of the invention for the expression of EbpA2 is a 130 kD receptor tyrosine kinase that is expressed at adherent idead binding causes autophosphorylation, however EbpA2 catherent idead of the invention of eliciting an immune response against an EbpA2 cappessing cell in a subject, involves administering to a subject composition comprising a Listeria bacterium that expresses an EbpA2 antigen peptide-expressing clieratia bacterium that expresses an EbpA2 antigen peptide-expressing Listeria bacterium, to treat a byperproliferative disorder of EbpA2-expressing cells, involving administering to the subject a composition comprising an unan subject having a disease involving betrant angiogenesis. Involving administering to the subject a composition comprising EbpA2 antigen peptide-expressing Listeria bacterium, to treat disease involving administering to the subject a composition comprising EbpA2 antigen Catherent angiogenesis. The method of the invention is useful for a cancer is a cancer of skin, lung colon, or peptide-expressing listeria bacterium, to treat disease involving an immune response against an EphA2-expressing cell in a subject having a listerial acancer is a cancer of skin, lung colon, or cast, prostate, bladder or pancresses of sacror of skin, lung colon, cargin or T cell origin. The cancer is a cancer of skin, lung cancer is a cancer of skin, lung cancer is a leader and sebbrachesic desactive disorder of EbpA2-expressing cells. The thyerproliferative disease involving a human subject having a bulbos
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                                                                                       Eliciting an immune response against EphA2-expressing cells in subjects, by administering composition comprising Listeria bacterium that expresses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    systemic lupus, psoriatic arthropathy, Reiters' syndrome, and Sjogrens' syndrome, endometriosis, preeclampsia, atherosclerosis or coronary artery
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                                                                                     cells in subjects,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9132 GGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGGA
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                                                                                                                                                                              Disclosure; SEQ ID NO 43; 219pp; English.
                                                                                                         by administering composition comprisi
EphA2 antigenic peptide, to subject.
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Kiener PA,
                                           WPI; 2005-322763/33.
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9012 TTCGAATTTCTGCCATTCATCGCTTATTATCACTTATTCAGGCGTAGC-ACCAGGCGTT 8954

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cassette

pAM401/pPL2 containing hly promoter/p60 sig pep.

Vector

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               9833 TGAATCGCCAGCGCATCAGCACCTTGTCTTGTCGCTATAATATTTGCCCATGGTGAAA
                                                                                                                                                                                           8773 ACGGGGGGGGAAGATGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
                                                                                                                                                                                                                                                        TGGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAA
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                                                                         8893 TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAGACGCATGAACC
                                                                                                                 TGAATCGCCAGCGCCATCAGCACCTTGTCGCCTTGCGTATATATTTGCCCATGGTGAAA
                                                                                                                                                                          470 ACGGGGGGGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
                                                                                                                                                                                                                                    CAGGGATTGGCTGAGACGAAAAACATATTCTCAATAAACCCTTTAGGGAAATAGGCCAGG
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AEB80052 standard; DNA; 9808

AEB80052/

06-OCT-2005 (first entry)

AEB80052;

XXXX

The invention relates to a recombinant nucleic acid molecule (1) acid bacterium, where (A) is codon-optimized for expression in the bacterium, where (A) is codon-optimized for expression in the bacterium, where (A) is codon-optimized for expression in the bacterium, and a second polymortal (B) encoding a polypeptide, where (B) is in the same translational reading frame as (A), where (A) encodes a fusion protein comprising the signal peptide and the polypeptide). Also comprising (I) and (B), a recombinant Listeria bacterium (II) comprising or treating a roadition in a host (comprising II), a method of preventing or treating a condition in a host (comprising II), a cecombinant Listeria bacterium (II), a cassette. The polypeptide encoded by (B) comprises an antigen (a tumor-associated antigen, an infectious disease antigen, or a polypeptide derived from an infectious disease antigen, or a polypeptide derived from an infectious disease antigen, or a polypeptide derived from an infectious disease antigen, or a polypeptide derived from an infectious disease antigen, or a polypeptide derived from an infectious disease antigen, or a polypeptide derived from an infectious disease antigen, or the bisteria bacterium, or both. The signal peptide from Listeria monocytogenes or is a p60 signal comprises human mesothelin deleted of its signal peptide and C(I) elsterial peptide and C(C) emplesses human mesothelin deleted of its signal peptide and companies the compinant bacterium is useful in the manufacture of a mantigen, and immune response in a host to an antigen, and animaniman in a host to an antigen is comprises human mesothelin deleted of its signal peptide and condition is a host to an antigen and animanimal mesothelin deleted of its signal peptide and condition is a host to an antigen or treating as useful in the manufacture of an encoded by the comprise and an immune response in a host to an antigen and antigen cancer, infections and autoimmunity. The recombinant nucleic acid molecule, expression casettes and vectors are useful for expressing and/or secreting polypeptides including heterologous polypeptides auch as antigens in bacteria. The present sequence represents the Vector pAM401 which contains the hly promoter/p60 signal peptide cassette. New recombinant nucleic acid molecule (comprising a first polynucleotide encoding a signal peptide native to a bacterium; and a second polynucleotide encoding a polypeptide) useful e.g. to induce immune response in host to antigen. The invention relates to a recombinant nucleic acid molecule (I) Vector; ds; listeriolysin O; Cytostatic; Antimicrobial; Immunosuppressive; Immunostimulant; vaccine; fusion protein; protein production; protein secretion; immune response; cancer; infection; autoimmune disease. Cook DN; Example 13; SEQ ID NO 33; 271pp; English. Luckett WS, 2004US-0541515P. 2004US-00773618. 2004US-00773792. 2004US-0556744P. 2004US-0599377P. 2004US-0615287P. 2004WO-US023881 23-DEC-2004; 2004WO-US044080 06-OCT-2004; 2004US-0616750P Portnoy DA, monocytogenes WPI; 2005-534010/54. (CERU-) CERUS CORP. WO2005071088-A2. 06-FEB-2004; 26-MAR-2004; 30-JUN-2004; Dubensky TW, Unidentified. 23-JUL-2004; 06-FEB-2004; 05-AUG-2004; 02-FEB-2004; 04-AUG-2005 Synthetic Listeria

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24-DEC-2003; 2003US-0532696D.
18-AUG-2004; 2004US-060258BP.
01-OCT-2004; 2004US-061554BP.
07-OCT-2004; 2004US-0617564P.
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                                                                  1070 ACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCAGGGCTTCCCGGTATCAACA
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Unidentified.
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Eliciting an immune response comprises administering to an individual a composition comprising an Eph2 antigenic peptide, an Eph2 antigenic peptide expression vehicle, or antigen presenting cells.

Disclosure, SEQ ID NO 43; 241pp; English.

The invention relates to a method of eliciting an immune response against an Eph2-expressing cell. The method comprises administering to an individual a composition comprising an Eph2 antigenic peptide, an Eph2 antigenic peptide expression vehicle, antigen presenting cells sensitized with an EphA2 antigenic peptide, or an anti-idiotypic antipody or its antigen-binding fragment, which immunospecifically binds to an idiotype of an anti-EphA2 antibody, in an amount to elicit an immune response against an EphA2-expressing cell. Also described are: (1) a method of treating a human individual having a hyperproliferative disorder of an EphA2-expressing cell, or a disease involving aberrant angiogenesis, comprising performing the method of the invention; and (2) a method of administering them to an individual as an EphA2 vaccine. In the method of

The invention, the kppak antiguing peptide is not any of the sequences given as SEQ in the specification. The composition further comprises an adjuvant, a heat shock protein bound to the Bph2 antigenic peptides. The expression vehicles expressing the Bph2 antigenic peptides. The expression vehicles expressing the Bph2 antigenic peptides. The expression vehicle is an infectious agence encoding the Bph2 antigenic peptide operably linked to a promoter, where the sequence antigenic peptide operably linked to a promoter, where the sequence conditions the infectious agent. The method of the invention is useful for treating a human individual having a hyperproliferative disorder of Bph2.

The expressing cells by administering to the individual a composition comprising antibodies produced by administering an Bph42 vaccine to a composition comprising an Bph42 expression cells. Alternatively, the individual can be administered with a composition comprising an Bph42 expression vehicle, e.g. bacterium or virus, in an amount to treat a hyperproliferative disorder of Bph42.

Expressing cells, and administering to the individual an antibiotic or antiviral agent in an amount to treat a bacterial or viral infection. The methods and compositions of the invention are useful for eliciting an immune response against an BphA2-expressing cell, and for treating a contract of the skin, the contract of renal cell carcinoma or melanoma), a non-neoplastic hyperproliferative disorder (e.g. an epithelial cell disorder, specifically asthma, chronic pulmonary obstructive disease, lung fibrosis, bronchial hyper responsiveness, psoriasis, or seborrheic dermatitis), or a disease involving aberrant anglogenesis (e.g. macular degeneration, diabetic retinopathy, retinopathy of prematurity, vascular restenosis, infantile hemangioma, verruca vulgaris, Kaposi's sarcoma, neurofibromatosis, recessive dystrophic epidermolyysis bulloas, rheumatoid arthritis, ankylosing spondylitis, systemic lupus, psoriatic arthropathy, Reiter's syndrome, and Sjogren's syndrome, endometriosis, preeclampsia, atheroscierosis or coronary artery disease). This sequence represents a plasmid containing a multiple cloning site (MCS). It is used in the exemplification of the method of the invention. lung, colon, ovary, esophagus, breast, prostate, bladder or pancreas or invention, the EphA2 antigenic peptide is NOT any of the sequences

Sequence 9808 BP; 2836 A; 1923 C; 1946 G; 3103 T; 0 U; 0 Other;

9133 9013 9073 8954 8893 TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAGACGGCATGATGAAGC 8834 8773 ACGGGGGGAAGAAGTTGTCCATATTGGCCACGTTAAATCAAAACTGGTGAAGTCAAC 8714 109 8953 TAAGGGCACCAATAACTGCCTTAAAAATTACGCCCCGGCCCTGCCACTCATCGCAGTAC 8894 3833 TGAATCGCCAGCGCATCAGCACCTTGTCGCCTTGCGTATATATTGCCCATGGTGAAA 8774 229 289 409 469 169 290 TAAGGGCACCAATAACTGCCTTAAAAAATTACGCCCCGCCCTGCCACTCGTCGCAGTAC 349 ACGGGGGGGAAAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC 529 110 GGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAAACCAGGA 9072 ATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGACCGGGTCGAATTTGCT 50 AAAACGGATCCTATCGTCAATTATTACCTCCACGGGGAGGCCTGAGCAAACTGGCCTCA 9192 ATAAATGATCATATATCATCACGGGGAGAGCCTGAGGAAACTGGCCTCA 9132 GGCATTTGAGAAGCACACGGTCACATTCCGGTAGTCAATAAACCGGTAAAACCAGCA 170 ATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGACGGGTCGAATTTGCT 230 TTCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT 9012 Trcgaartrcrgccarrcarccccrrarrarcacrrarrcaggcgrage-accaggcgrr TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACC TGAATCGCCAGCGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAA Gaps 1; 89.0%; Score 1116; DB 14; Length 9808; 98.6%; Pred. No. 0; Indels 0; Mismatches 15; Best Local Similarity 98.6 Matches 1136, Conservative 350 410 470 Query Match g ò g ò 셤 δ a ઠે g ઠે g ઠે 셤

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                                                                                                       2332 TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAGAGGCATGATGAAGC
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TTCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT
                     2213 TTCGAATTTCTGCCATTCATCCGCTTATTATCAATTATTCAGGCGTAGC-ACCAGGCGTT
                                                                               TAAGGGCACCAATAACTGCCTTAAAAAATTACGCCCCGCCCTGCCACTCATCGCAGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of the plasmid pRZTL1 which is used to demonstrate in vitro transposition of a transposable element located between a pair of Tn5 (transposen 5) outside end (OB) termini. The invention provides a genetic construct that contains a nucleotide sequence encoding a modified Tn5 transposase enzyme that has both greater avidity for Tn5 OB repeats and is less likely to assume an inactive multimeric form than a wild type Tn5 transposase and a transposable DNA sequence flanked at its 5' and 3' ends by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A at position 10, T at 11 and A at 12. DNA sequence comprising nucleotide A at position 10, T at 11 and A at 12. The modified Tn5 transposase and the transposable DNA which is a DNA chonce molecule are used in a system for in vitro transposation. The system and method can be used to create absolute defective mutants, to provide selective markers to target DNA, to provide portable regions of homology to a target DNA, to facilitate insertion of specialised DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences into target DNA, to provide primer binding sites or tags for DNA sequences into ther desired combinations of DNA sequences (combinatorial content easired combinations of DNA sequences (combinatorial content easired combinations of at least about 100-fold higher than tanker because the transposase facilitates in vitro
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88.9%; Score 1114.4; DB 2; Length 5838;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1135; Conservative 0; Mismatches 16; Indels 1;
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"chloramphenicol resistance"
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/note= "kanamycin resistance"
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P-PSDB; AAW56695, AAW56696, AAW56697.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                              cransposase; modified form; wildtype; multimeric; OE termini; IE termini;
outside end termini; inside end termini; plasmid; repeat sequence;
mutation; cyclic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This plasmid can be used in the assay of transposition frequency by the modified Th5 transposase. The insertion of the Th5 transposase releases a fragment of the plasmid that corresponds to the region of Kanamycin resistance gene that lies between the two OB sequences. The plasmid was also used to investigate the nature of the termini involved in the transposition reaction. Wildtype Outside End (OB,AA206435) and Inside End (IE, AA206439) were compared and an effort made to randomise the nucleotides at each of the seven positions of difference. This eventually lead to the identification of the mutant OB sequences AA206435 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0 U; 0 Other;
                                                                                                                                                                                                                                      /function= "acetylates chl"

/product= "chloramphenicol acetyltransferase"

(function= "acetylates chl"

function= "acetylates chl"

/phenotype= "chloramphenicol resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In vitro transposition using a Tn5 based genetic construct.
                                                                                                                                                                                                                                                                                                1715. .5530
/*tag= e
function= "blocks action of kanamycin"
                                                                                                                                                                           function= "effluxes tet"
product= "inner membrane protein"
phenotype= "Tetracycline resistance"
                                       Plasmid pRZTL1, target DNA for In5 transposase assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5838 BP; 1370 A; 1525 C; 1516 G; 1427 T;
                                                                                                                                                                                                                                                                                                                               /phenotype= "kanamycin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reznikoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY15383, AAY15384, AAY15385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Col 31-39; 48pp; English.
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            York DL, Goryshin IY,
                                                                                                                                     /*tag= a
77. 1267
/*tag= b
/gene= "TetR"
                                                                                                                                                                                                                      *tag= c
gene= "ChlR"
                                                                                                                                                                                                                                                                                                                                                                                                                                        (WISC ) WISCONSIN ALUMNI RES
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/*tag= d
                  (first entry)
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/*tag=
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                                                                                                                            insertion_seq
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                                                                                                                                                                                                                                                                                                                                    TTCGAATTTCTGCCATTCATCCGCTTATTATCAATTATTCAGGCGTAGC-ACCAGGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2272 TAAGGGCACCAATAACTGCCTTAAAAAATTACGCCCCGCCCTGCCACTCATCGCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2392 TGAATCGCCAGCGGCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCATGGTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2452 ACGGGGGGGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACC
TITICACCGIAACACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAATCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2752 TGAGCATTCATCAGGCGGGCAAGAATGTGAATAAAGGCCGGATAAAACTTGTGCTTATTT
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                                                                                           GGCATTTGAGAAGCACACAGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAAACCAGCA
                                                                                                                                                                        170 ATAGACATAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGGACCGGGTCGAATTTGCT
                                                                                                                                                                                                                ATAGACATAAAGCGGCTATTTAACGACCCTGCCCTGAACCGACGACCGGTCGAATTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACTCAAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCCAGGGCTTCCCCGGTATCAACA
                                                          GGCATTTGAGAAGCACACGGTCACACTGCTTCCGGTAGTCAATAAACCGGTAAACCAGCA
                                                                                                                                                                                                                                                                                                TTCGAATTTCTGCCATTCATCCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAATCGCCAGCGCCATCAGCACCTTGTCGCCTTGCGTATAATATTTGCCCCATGGTGAAA
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Query Match 88.9%; Score 1114.4; DB 2; Length 5838; Best Local Similarity 98.5%; Pred. No. 0; Matches 1135; Conservative 0; Mismatches 16; Indels 1;

1;

1; Gaps

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Search completed: January 17, 2006, 19:35:10 Job time : 784.788 secs

Run on:

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CL114392 ISB1-60C1
CL1134505 ISB1-105B
DU053555 141229 TO
CL1039461 CR216-470
CL111697 ISB1-60F2
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CL112625 ISB1-57G1
CL112625 ISB1-57G1
CL12451 ISB1-101K
CL12451 ISB1-102K
CL12451 ISB1-102L
CL132916 ISB1-102L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 971)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .971
| Organism="Xenopus tropicalis" |
| /organism="Xenopus tropicalis" |
| /organism="Xenopus tropicalis" |
| /organism="Sype="genomic DNA" |
| /organ="ISB1-55D1" |
| /olone="ISB1-55D1" |
| /olone="Wettor: pBeloBAC11; ISB-1 Xenopus tropicalis BAC |
| Library Segment 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 TCGAATTTCTGCCATTCATCCGCTTATTATCACTTTATTCAGGCGTAGCAACCAGGCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 8.6e-254;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Mashington University School of Medicine
Email: submissionsewatson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
(lass: BAC ends
High quality sequence start: 8
High quality sequence stop: 824.
Location/Qualifiers
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                           CL114392
CL132776
CL0329461
CL0329461
CL114498
CL1344387
CL1344387
CC279944
CL112625
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CL112636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CL111359 ... GI:40604994
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ilarity 99.1%;
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/clone="lbb="ISB1"
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                   genome
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Washington University School of Medicine
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                                                                                                 Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seg primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 2
High quality sequence stop: 744.
Location/Qualifiers
Mardis, E. and Wilson, R.
A physical map of the xenopus
Unpublished (2003)
Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 96.4
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1 (bases 1 to 1039)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
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Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Ambabbia: Butachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

I (bases I to 988)

Xremizaki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

Umpublished (2003)

Contact: Richard K Wilson
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                      302 CACATCTTGCGAATATATGTGTAGAAACTGCCGGAAATGGTCGTGGTATTCACTCCAGAG
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Washington University School of Medicine
Bmail: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
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SM Xenopus tropicalis (western clawed frog)

SM Xenopus tropicalis

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

E i (bases 1 to 973)

SK Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

L Unpublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine
Email: submissions@watson.wustl.edu

Insert Length: 75000 $td Error: 0.00

Seq primer: T7 TAATACGACTCACTATAGGG

Class: BAC ends

High quality sequence statt: 2

High quality sequence stop: 769.
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CL112191.1 G1:40605826
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/clone="ISB1-56K13"
/clone lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
                                 TGGTATATCCAGTGATTTTTTTCTCCATTTTTAGCTTCCTTAGCTCCTGAAAATCTCGACA
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(bases 1 to 994)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
Unpublished (2003)
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/clone lib="ISB1"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis
Library Segment 1"
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                       1113
                                                                  968
                                             926 ACGIGGCGATC-ACGICTCATTITCGCCAAAGIIGGCCCAAGG
                       1070 ACGIGCCGAICAACGICTCAITITCGCCAAAAGIIGGCCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 6
High quality sequence stop: 804.
                                                                                                                                                                                                                                                                                                                Xenopus tropicalis (western clawed frog)
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/organis="Xenopus tropicalis"
/mol_type="genomic DNA"
/db_xref="taxon:8364"
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Class: BAC ends
High quality sequence start: 16
High quality sequence stop: 847.
High quality sequence stop: 847.
Location/Qualifiers
1. 968
| / organism="xenopus tropicalis"
| / mol_type="genomic DNA"
| / db xref="tash=101415"
| / clone="ISB1-101415"
| / clone="Lib="ISB1"
| / note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC Library Segment 1"
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Pred. No. 4.5e-249;
0; Mismatches 5;
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1 (bases 1 to 1001)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

A phyaical map of the xenopus tropicalis genome
Unpublished (2003)
121 CTTTCATTGCCATACGGAATTCCGGATGAGCATTCATCAGGCGGCGAGAATGTGAATAA 480
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Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTATAAGG
Class: BAC ends
High quality sequence start: 10
High quality sequence stop: 776.
Location/Qualifiers
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AUTHORS
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                                                                                                                                                          Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1047)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
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Library Segment 1"
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.larity 97.7%; Pred. No. 9e-245;
Conservative 0; Mismatches 20; Indels 0;
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Mashington University School of Medicine
Email: submissions@wateson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
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High quality sequence stop: 769.
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                                                                                                                             CL091480.1 GI:40585115
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AUTHORS
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                      RESULT 7
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SOURCE Xenopus tropicalis (western clawed frog) ORGANISM Xenopus tropicalis Eukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi,	Xenopodinae; Xenopus; Silurana. REFERENCE 1 (bases 1 to 971) AUTHORS Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,	Mardis, E. and Wilson, K. TITLE A physical map of the xenopus tropicalis genome JOURNAL Unpublished (2003) COMMENT Contact: Richard K Wilson	Genome Sequencing Center Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Length: 75000 Std Error: 0.00	Seq primer: T/ TAATACGACTCACTATAGGG Class: BAC ends High quality sequence start: 10 High quality sequence stop: 786.	<pre>FEATURES Location/Qualifiers 1. 971 /organism="Xenopus tropicalis" /mol_type="genomic DNA"</pre>	/db_xref="taxon:8364" /clone=1881-97189" /clone=11b=17891" /note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC	orary segme	Best Local Similarity 97.3%; Pred. No. 9.2e-243; Matches 877; Conservative 0; Mismatches 21; Indels 3; Gaps 3; Ov 284 GGCGTTTBAGGGCACTARTAACTGCCTTBAAAAAATTACGCCCGCCCGCCTGCCTATGG 343	3 GETTITIAAGGCACCAATAACTGCCTIAAAAAATTACGCCCCGCCC		OY 404 TGAACCTGAATCGCCAGCGGCATCAGCACTTGTCGCTTGCGTATAATATTTGCCCATG 463	Oy 464 GTGAAAACGGGGGGAAAAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAA 523	Db 183 GTGAAAACGGGGAAGAAGTTGTCCATATTGGCCACGTTTAAATCAAAACTGGTGAAA 242 Qy 524 CTCACCCAGGGATTGGCTGAAACGAAAAAACTATTCTCAATAAACCTTTAGGGAAATAG 583	243 CTCACCCAGGGATTGGCTGAGACGAAAACATATTCTTTTTTTT	Qy 584 GCCAGGTTTTCACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAACTGCCGGAAA 643	Oy 644 TCGTCGTGGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTG 703		Oy . 704 TAACAAGGGTGAACACTATCCCATATCACCAGGTCACGGTCTTTCATTGCCATAAT 763 Db 423 TAACAAGGGTGAACACTATCACCAGTCAGCTCATTGCCTTTGCATTGCGAAA 482	
Oy 231 TCGAATTTCTGCCATTCATCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGGTTT 290	Oy 291 AAGGGCACCAATAACTGCCTTAAAAAATTACGCCCCGCCTGCCACTCATCGAGTACT 350	Qy 351 GTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACCT 410	OY 411 GAATCGCCAGGGCATCAGCACTTGTCGCCTTGCGTATATTTTGCCCATGGTGAAAA 470	OY 471 CGGGGGGGAAGAAGTIGTCCATAITGGCCACGTTTAAATCAAAACTGGTGAAACTCACCC 530	Qy 531 AGGGATTGGCTGAGACGAAAACATATTCTCAATAAACCCTTTAGGGAATAGGCCAGGT 590	OY 591 TITCACCGTAACACGCCACATCTTGCGAATATATGTGTAGAAAACTGCCGGAAATCGTCGT 650	Qy 651 GGTATTCACTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAAGA 710	Oy 711 GGTGBACACTATCCCATATCACCACTCACGGTCTTCATTGCCATACGTAATTCCGGAT 770 Db 567 GGTGBACACTATCCCATATCACCAGGTCACGGTCATTCATTGCATTCCGGAT 626	GAGCATTCATCACGGGGCGAGAATGTGAATAAAGGCCGGATAAAACTTGTGCTTATTTT 	831 TCTTTACGGTCTTTAAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAGGTACATT	Db 687 TCTTTACGGTC-TTAAAAGGCCGTAATATCCAGCTGAACGGTTAATAGGTACATT 745 Qy 891 GAGCAACTGAAAATGCCTCAAAATGTTCTTTACGATGCCATTGGGATATATCAACGG 950		OY 951 TGGTATATCCAGTGATTTTTCTCCATTTTAGCTTCCTTAGCTCCTGAAAATCTCGACA 1010 	1011 ACTCAAAAATACGCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAACCTCTTA	Db 865 ACTCAAAAA-ACGCCCGGGGTGATCTTTTTTTTTGGGGAAAGTGGGAAACTCTTTA 923 Qy 1071 CGTGCCGATCAACGTCTCATTTTCGCCAAAAGTTGGCCCCAGGGCTTCCCGGTATCAACAG 1130		Qy 1131 GGACACCAGGATTTATTT 1148	Db 983 GGACCCCGGGATTTTT 1000	RESULT 9 CL129946 LOCUS CL129946 CL129946 DEFINITION ISBI-97H8_T7.1 ISBI Xenopus tropicalis genomic clone ISBI-97H8, genomic survey sequence.

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543 TTATTTTTTTTTTATAAAGGCCGTAATATCCAGCTGAACGGTCTGGTTATAG 602
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|Ste="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
| brary Segment 1"
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Carter, J., McPherson, J., Warren, W., ad Wilson, R. and of the xenopus tropicalis genome (203) that K Wilson
                                                                                              nncing Center
Nniversity School of Medicine
ssions@watson.wustl.edu
hi: 75000 Std Error: 0.00
T7 TAATACGACTAATAGGG
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1 type="genomic DNA"

xref="taxon:8364"
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sequence stop: 786.
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S. S. S. C. C. C.

CL129946 15B1 Xenopus tropicalis genomic clone ISB1-97H8, genomic survey sequence.
CL129946.1 GI:40623581 6SS 05-JAN-2004 6SS.

ACCESSION VERSION KEYWORDS

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tropicalis genomic clone ISB1-57C16,
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Xenopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1007)

1 (bases 1 to 1007)

Markins, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome
                                                                                                                                                                                                                                                                                                                                             266 GAATGGCCAGCGGCATCATTACCTTGTCGTTTGCGTATAATATTTGCCCATGGTGAAAA
                                                                                                                                                                                  CGGGGGCGAAGAAGTTGTCCCATATTGGCCACGTTTAAATCAAAACTGGTGAAACTCACCC
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                                                                        GTTGTAATTCATTAAGCATTCTGCCGACATGGAAGCCATCACAAACGGCATGATGAACCT
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Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Ambibibia; Metazoda; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

I (bases I to 968)

Xremitaki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

Aphysical map of the xenopus tropicalis genome

Umpublished (2003)

Contact: Richard K Wilson
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                  663 TCAACGGTGGTATATCCAGTGATTTTTTTTCTCCATTTTAGCTTCCTTAGCTCCTGAAAT
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 8
High quality sequence stop: 751.
Location/Qualifiers
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|mol_type="genomic DNA"
|db_xref="taxon:8164"
|clone="ISB1-101C13"
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Contact: Bernd Weisshaar
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| Moal type="genomic DNA" |
| Moal type="genomic DNA" |
| Ab xref="taxon:834" |
| Clone="ISB1-57C16" |
| Clone lib="ISB1" |
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Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 8
High quality sequence stop: 801.
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larity 95.4%; Pred. No. 1.1e-240;
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Yellows Innear GSS 09-AUG-2005 KBrH124J09 genomic clone, KBrH (HindIII) BAC library Brassica rapa subsp. pekinensis, genomic survey sequence. 1068 TACGTGCCGATCAACGTCTC--ATTTTCGCCAAAAGTTGGCCCCAGGGCTTCCCGGTATCA 1126 ö 290 186 350 246 922 923 TACGGGCCGATTAAAGTCTCCATTTTCCCCAAAAGTTTGCCCCAGGGCTTCCCCGGTTTC 982 Brassica rapa subsp. pekinensis Brassica rapa subsp. pekinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. generated Direct Submission Submitted (09-AUG-2005) Weisshaar B., Bielefeld University, Institute for Genome Research, Universitaetsstrasse 25, D-33594 Bielefeld University, Institute for Genome Research Universitaetsstrasse 25, D-33594 Bielefeld, Germany Email: Dernd.weissbaar@uni-bielefeld.de BAC end sequences of Brassica rapa BAC clone KBrH124J09; genera as contribution to the 'Multinational Brassica rapa Sequencing Project' Seq primer: m13f TGTAAAAGGACGGCCAGT 1010 AACTCAAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAA-CCTCT 863 AACTCAAAAATACGCCCGGGAAGTGATCTTAATTCATTATGGGGAAAGTTGGAACCCTCT TCGAATTTCTGCCATTCATCGCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTTT Gaps /sub_species="pekinensis" /db_xref="taxon:51351" /clone="XBTH124409" /clone_lib="KBrH, Brassica rapa HindIII BAC library GF-SCF-1002, Vector: pCUGlBac1" /lab_host="B.coli DH108" ö DB 11; Length 945; /organism="Brassica rapa subsp. pekinensis" /mol_type="genomic DNA" /strain="Chiifu type 401-42" /cultivar="Chiifu" IndelB Viehoever,P., Holtgraewe,D. and Weisshaar,B. BAC end sequences of Brassica rapa Unpublished Score 815.8; DB 11; Pred. No. 5.5e-238;); Mismatches 2;

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/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/db xref="taxon:8364"
/clone="ISB1-101N19"
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/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
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Pred. No. 2e-237;
0; Mismatches 5;
Seg primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 12
High quality sequence stop: 877.
Location/Qualifiers
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                                                          ATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAACAAGGGTGAACACTATCCCATA 438
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Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

I (bases 1 to 901)
Kremitski,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Washington University School of Medicine
Basil: submissions@watson.wustl.edu
Insert Length: 75000 Std Brror: 0.00
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
High quality sequence start: 18
High quality sequence stop: 734.
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Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

Berartos; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

E (bases 1 to 952)

Mueller,L.A., Buels,R.M., Wang,Y., Tanksley,S.D., Giovannoni,J.J.,

Van Eck,J. and Stack,S.

BAC end sequencing from three Solanum lycopersicon libraries

L Unpublished (2005)

Other GSSs: 254990

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Cornell University.

251 Emerson Hall, Ithaca, NY 14853, USA

Tel: 607-255-6687

Fax: 607-255-6687

Email: sgn-feedback@sgn.cornell.edu

Plates: 34 row: N column: 17
                                                                                       311863 Tomato EcoRI BAC Library Lycopersicon esculentum genomic clone SL EcoRI0034N17 5, genomic survey sequence.
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869 ACTC-AAAAATACGCCCGGTAGTGATCTTATTTCATTATGGTGAAAGTTGGAAC 921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Lycopersicon esculentum"
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/db_xref="taxon:4081"
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/clone_lib="Tomato EcoR1 BAC_Library"
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High quality sequence start: 19
High quality sequence stop: 680.
Location/Qualifiers
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                                                                                              TAAGGGCACCAATAACTGCCTTAAAAAATTACGCCCCGCCCTGCCACTCATCGCAGTAC
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                                                       TTCGAATTTCTGCCATTCATCGCCTTATTATCACTTATTCAGGCGTAGCAACCAGGCGTT
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                  Length
                64.1%; Score 803.6; DB 10; Length
96.7%; Pred. No. 3e-234;
ive 0; Mismatches 24; Indels
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                                     Conservative
                           Similarity
                                     Matches 853;
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AY781401 Synthetic
AY781408 Synthetic
AY781408 Synthetic
AY781403 Synthetic
AY781403 Synthetic
AY781407 Synthetic
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AY781402 Synthetic
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AY781399 Synthetic
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main:jan,D.C., Casadaban,M.J., Weber,J.Mark. and Gaines,G.L. III.
Protein fusion method and constructs
Patent: US 5981177-A 6 09-NOV-1999;
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Unclassified.
1 (bases 1 to 71)
Demirjian,D.C., Casadaban,M.J., Weber,J.Mark. and Gaines,G.L. III.
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/organism="unknown"
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Sequence 6 from patent US 5981177.
AR084420
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BD073246 In vitro
AR35386 Sequence
AR084418 Sequence
AR084417 Sequence
AR084417 Sequence
AR084417 Sequence
M12560 Synthetic
M12582 Mu-derived
M34920 Bacteriopha
M34920 Bacteriopha
M35723 Escherichia
M35728 Broberichia
AR781404 Synthetic
AR781404 Synthetic
AR781405 Synthetic
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                                                                                                             ; Search time 257.623 Seconds (without alignments) 11032.288 Million cell updates/sec
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OS Artificial Sequence

NO 19 2001510055-A/1

PD 31-JUL-1998 JP 2000503240

PR 10-JUL-1997 RI 972392

PR 14-JUL-1997 RI 972392

PR THOMAS TENKANEN, TIMO SOININEN, HARI SABIRARTY, KIRSI MURTANEN PC

C12Q1/68,C12N15/09,C12N15/00

CC Description of Artificial Sequence: transposon DNA capable of
                                                                                                                                                                                                                                                                          BD073246 17 bp DNA linear PAT 27-AUG-2002 In vitro method for providing template for determination of DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                         Tenkanen, T., Soininen, T., Sabirarty, H. and Murtanen, K.
In vitro method for providing template for determination of DNA
Patent: JP 2001510055-A 1 31-JUL-2001;
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                                                                                                                  Score 39.4; DB 6; Length 71;
Pred. No. 0.005;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                 synthetic construct
synthetic construct
sher sequences; artificial sequences.
1 (bases 1 to 77)
Protein fusion method and constructs
Patent: US 5981177-A 5 09-NOV-1999;
Location/Qualifiers
                                                                                                                                              0; Mismatches
                                           1. .71
/organism="unknown"
/mol_type="unassigned DNA"
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JP 2001510055-A/1.
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1 Similarity 97.6%;
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Unclassified.
1 (bases 1 to 77)
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Best Local Similarity
Matches 40; Conserv
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Matches 40; Conserv
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BD073246
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PMUBSR 82 bp DNA linear PHG 28-APR-1993
Bacteriophage Mu right end with Mu A protein binding site R3.
M10177
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Site-specific recognition of the bacteriophage Mu ends by the Mu A
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Unclassified.
Unclassified.

L (bases I to 83)

Demirjian, D.C., Casadaban, M.J., Weber, J.Mark. and Gaines, G.L. III.

Protein fusion method and constructs

Patent: US 5981177-A 4 09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craigie,R.
Unpublished (1985)
Original source text: Bacteriophage Mu DNA.
Computer-readable sequence for [1] kindly provided by R.Craigie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no RNA stage; Caudovirales; Myoviridae;
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Tenkanen,T., Soininen,T., Savilahti,H. and Multanen,K.
In vitro method for providing templates for DNA sequencing
Patent: US 6593113-A 1 15-JUL-2003;
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/organism="Enterobacteria phage Mu"
/mol type="genomic DNA"
/db_xref="taxon:10677"
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                                                                                                                                                                                                                                                                                1;
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ligie, R., Mizuuchi, M. and Mizuuchi, K.
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Pred. No. 0.005;
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Sequence 4 from patent US 5981177.
AR084418.1 GI:10011189
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/organism="unknown"
/mol_type="genomic DNA"
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                                                                                                        Location/Qualifiers
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Enterobacteria phage Mu
Viruses, dsDNA viruses,
Mu-like viruses.
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1 Similarity 97.6%;
40; Conservative (
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PHG 28-APR-1993

DNA

FEATURES

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мсмизк
Mu-derived phage lambda placMu3 provirus right end (MuR) inserted
in pBRG1214.
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Enterobacteria phage Mu
Viruses, dsDNA viruses, no RNA stage, Caudovirales, Myoviridae,
Mu-like viruses.
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Enterobacteria phage Mu
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
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Pred. No. 0.0048;
0; Mismatches 1; Indels
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15 GCACGAAAAAGCGCGAAAGCGTTTCACGATAAATGCGAAAAC
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/organism="Enterobacteria phage Mu"
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Location/Qualifiers
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1 (bases 1 to 220)
Nag, D.K. and Berg, D.E.
Specificity of bacteriophage Mu excision
Mol. Gen. Genet. 207 (2-3), 395-401 (1987)
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                                                                                                      150 bp DNA Bacteriophage Mu DNA, SE end fragment. M10863
                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences at the ends (Nature 274 (5671), 553-558 (1978) 672985
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db xref="taxon:10677"
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/db_xref="taxon:10677"
1. .220
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/note="right end"
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Best Local Similarity 97.6%;
Matches 40; Conservative 0
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Demirjian,D.C., Casadaban,M.J., Weber,J.Mark. and Gaines,G.L. III.
Protein fusion method and constructs
Patent: US 5981177-A 3 09-NOV-1999;
Location/Qualifiers
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synthetic construct
other sequences, artificial sequences.

1 (bases 1 to 120)
Narang, S.A., Dubuc, G., Yao, F.L. and Michniewicz, J.J.
'In vitro' method of assembling a synthetic gene
Biochem. Biophys. Res. Commun. 134 (1), 407-411 (1986)
3004442
Original source text: Phophorylated synthetic DNA fragm
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78.8%; Score 39.4; DB 11; Length 120;
Best Local Similarity 97.6%; Pred. No. 0.0048;
Matches 40; Conservative 0; Mismatches 1; Indels 0.
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                                                                                                          78.8%; Score 39.4; DB 6; Length 83; larity 97.6%; Pred. No. 0.0049; Conservative 0; Mismatches 1; Indels
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Sequence 3 from patent US 5981177.
AR084417
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RESULT 8

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SYN 27-APR-1993

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E"
                                                                                                                                                                                                                                                                                                                          M15949.1 GI:209098
S synthetic sequence.
synthetic construct
ISM synthetic construct
other sequences; artificial sequences.

T hases 1 to 32.

B patterson, T.A., Court, D.L., Dubuc, G., Michniewicz, J.J.,
Goodchild, J., Bukhari, A.I. and Narang, S.A.
Transposition studies of mini-Mu plasmids constructed from the chemically synthesized ends of bacteriophage Mu
L Gene 50 (1-3), 101-109 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSION VECTOR FOR ADJUSTABLE EXPRESSION OF EXOGENOUS GENES IN
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/organism="synthetic construct"
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705. .78
/note="unnamed protein product; pNM506 mgl-B sequenz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 324;
                                                                                                               Score 39.4; DB 1; Length 240;
Pred. No. 0.0046;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                          324 bp DNA linear Synthetic Bacteriophage Mu left and right end DNA. M15949
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Location/Qualifiers
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Pred. No. 0.0045;
0; Mismatches 1;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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PACENT: WO 8809373-A 6 01-DEC-1988;
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/transl_table=11
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nilarity 97.6%;
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pNM506 DNA sequence.
A02708
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Metcalf, W., Steed, P.M. and Wanner, B.L.
Identification of phosphate starvation-inducible genes in
Escherichia coli K-12 by DNA sequence analysis of psi::lac2(Mu dl)
transcriptional fusions
J. Bacteriol. 172 (6), 3191-3200 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                             Enterobacteria phage Mu
Enterobacteria phage Mu
Enterobacteria phage Mu
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
Mu-like viruses
1 (bases 1 to 220)
Groenen,M.A., Timmers,E. and van de Putte,P.
DNA sequences at the ends of the genome of bacteriophage Mu
essential for transposition
Proc. Natl. Acad. Sci. U.S.A. 82 (7), 2087-2091 (1985)
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Nucleotide sequence of the alkaline phosphatase gene of
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Pred. No. 0.0046;
0; Mismatches 1; Indels
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Escherichia coli transposon Mu dl-R insertion site.
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/organism="Enterobacteria phage Mu"
/mol_type="genomic DNA"
/db_xref="taxon:10677"
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                                                                                     PMUNE2 220 bp Bacteriophage mu genomic right e
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3533724
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Best Local Similarity 97.6%;
Matches 40; Conservative (
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Escherichia coli
Escherichia coli
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LKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHFCYTVFHEQTETF
SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFLENMFFVSANPMVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
A"
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Synthetic construct transposon mini-Mu transposon TnCR6, complete
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Direct Submission
Submitted (14-OCT-2004) CopyRat Pty Ltd, 27-31 Wright Street,
Clayton, Victoria 3168, Australia
Location/Qualifiers
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                                                                                    ch 78.8%; Score 39.4; DB 6; Length 903; Similarity 97.6%; Pred. No. 0.0042; 40; Conservative 0; Mismatches 1; Indels
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/db_xref="G1:60171998"
/protein id="CAA00263.1"
/db_xref="GI:344653"
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                                                                                                                                                                              1. 1319
/transposon="mini-Mu transposon TnCR6"
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/mol_type="other DNA"
/db_xref="taxon:32630"
1. .1319
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synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1319)
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AY781404.1 GI:60171997
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Aad21278 Bacteriop

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Aad01008

Adl22564 Human dis

Aas98204 DNA encod Ads73196 Human kid Adw42050 cDNA elev

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Aak71665 Human imm
Aak64966 Human imm
Aak64964 Human imm
Ac138625 Rice etre
Abq71053 Listeria
Abq71053 Listeria
Continuation (10 o
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Adr85671 Aspergill
Adr85084 Aspergill
Adr8568 Aspergill
Adr85645 Oligonucl
Abq25452 Oligonucl
Abq32590 Oligonucl
Abq32590 Oligonucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposase the transposas is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by transposase useful for producing deletion derivatives of polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a transposon nucleic acid comprising a
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                                     AEB48763
AEB48763
AAS98204
ADS73196
ADW42050
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ABQ71053
ABQ69245
ABQ67197_(
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AAN80102
AAZ28877
AAD01008
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AAK64966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-2003; 2003WO-FI000285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2002; 2002FI-00000746.
                                                                                                                                                                                                                                                                                                                          ACF58172 standard; DNA; 50
                                                                                                                                                                                                                                                                                                                                                                 15-JAN-2004 (first entry)
                                                                   2229
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                                                                                                                            Synthetic.
Bacteriophage mu.
  NNNNN0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003087370-A1.
                                      23-OCT-2003
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 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Ad813821 Mu end DN
Aa221279 Precut tr
Acf58171 Cat+Mu (No
Acf58170 Cat-Mu (No
Acf58170 Cat-Mu tr
Ac8883 Mini-Mu t
Acc80745 Transposo
Acz28881 Mini-Mu t
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Acc80738 Transposo
                                                                ; Search time 31.092 Seconds (without alignments) 10717.687 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                            1 tgattgattgaacgaaaaac......ttcacgataaatgcgaaaac
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        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                          4996997 segs, 3332346308 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                              nucleic search, using sw model
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AAZ28881
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ADS13820
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Acc80742 Transposo Acc80753 Transposo Adr14827 PCR prime

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78 77 78 77 78 77 78 77 78 77 78

Score

Result Š Sequence 54 BP; 22 A; 9 C; 12 G; 11 T; 0 U; 0 Other;

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transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence recognized by a transposase; and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a Cat-Mu transposon modified end
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^*tag= a
/note= "the 5' end of this strand overhangs the 3'end
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                                                                                                                                                                                                                                            1 TGATTGATTGAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 10; Length 50; 100.0%; Pred. No. 9.5e-09; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transposon; genetic engineering; transposase; Cat-Mu; ds.
                                                                                                                                Sequence 50 BP; 21 A; 8 C; 11 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the complementary strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment.
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                                                                                                                                                                                                                                                                                                                                                                           BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-2002; 2002FI-00000746
                                                                                               fragment without 5' overhang
                                                                                                                                                                                                                                                                                                                                                                           ACF58168 standard; DNA; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to a transposon nucleic acid comprising a
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                                                                                                5 rgatrgatrgaacgaaaaacgcgaaagcgrtrcacgaraatgcgaaaac
                                                                   1 TGATTGATTGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
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 Length 54;
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                                Indels
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100.0%; Pred. No. 1.4e-08;
iive 0; Mismatches 0;
100.0%; Score 50; DB 10; 100.0%; Pred. No. 9.5e-09;
                                  Mismatches
                                                                                                                                                                                                                                                                                     Modified Cat-Mu(Stop)-transposon.
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                                                                                                                                                                                                                                                    (first entry)
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                                    Conservative
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Best Local Similarity
                 Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage mu.
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 Query Match
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ID ACF581
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ACF58169
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ACF58169;

Synthetic

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Any interaction trained or distributed or detecting a mismatch in a test double stranded nucleic acid transposition of the Mu-end nucleic acid into the target, where transposition at the predominant site indicates the presence of mismatch at about that site. The methods are useful for typing a pathogenic microorganism strain, for screening an embryo for the presence of mismatch microorganism strain, for screening an embryo for the presence of interest, detecting the presence of known mutation in a gene of interest, and diagnosing the presence or absence of a tumour-promoting mutation. The kit is useful for detecting the presence of a number of nucleic nor polymorphism of interest in a nucleic acid molecule. The oligonucleotide MM1141.
                                                                                                                                                                                                                                                                            Detecting a mismatch in a test double stranded nucleic acid target, useful for typing a pathogenic microorganism strain, comprises detecting transposition of the Mu-end nucleic acid into the target.
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of detecting a mismatch in a test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insertional mutation; synaptic complex; transposon; screening; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Precut transposon end of Bacteriophage Mu non-transferred strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.8%; Score 39.4; DB 13; Length 51; 97.6%; Pred. No. 7.5e-05; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
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                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 2; 24pp; English.
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97.68; Pr.
                                                              26-MAR-2004; 2004US-00809688.
                                                                                                    28-MAR-2003; 2003US-0457934P
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                                                                                                                                                                                       Yanagihara K, Mizuuchi
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                                                                                                                                               (USSA ) US SEC OF ARMY
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                    30-SEP-2004.
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28-JAN-2002
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Matches
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AAD21279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by a transposase useful for producing deletion derivatives of polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 50; DB 10;
Pred. No. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposon nucleic acid comprising
                                                                                                Modified Cat-Mu(Stop)-transposon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 30; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                         14-APR-2003; 2003WO-FI000285
                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2002; 2002FI-00000746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS13821/c
ID ADS13821 standard; DNA; 51
                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Savilahti H, Tieaho V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacteria phage Mu
                                                                                                                                                                                                                                                                                                                                                                                                                            (FINN-) FINNZYMES OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-845329/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embryo screening;
                                                                                                                                                                                                              Bacteriophage mu.
                                                                                                                                                                                                                                                    WO2003087370-A1.
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                                                          15-JAN-2004
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                                                                                                   The present invention relates to a method for making an insertional mutation at a random or quasi-random position in cellular nucleic acid in a aranger cell comprising introducing into the target cell a synaptic complex. The method is particularly useful for efficiently inserting a transposable polynucleotide at random or quasi-random locations in the chromosomal or extra-chromosomal nucleic acid of a target cell. The method may also be used for screening the genome of cells that comprise an insertional mutation that induces a phenotypic or genotypic change relative to the cells that are not subject to insertional mutagenesis. The present sequence is the precut transposon end of Bacteriophage Mu non-transferred strand, used in the exemplification of the invention. (Updated on 11-SEP-2003 to standardise OS field)
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/*tag= a
/note= "the 5' end of this strand overhangs the 3'end of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by transposase useful for producing deletion derivatives of polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a transposon nucleic acid comprising a genetically engineered translation stop signal in the three reading
Making an insertional mutations, especially useful for efficiently inserting a transposable polynucleotide in a target cell, comprises introducing into the target cell a synaptic complex.
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                                                                                                                                                                                                                                                                                                                                                                            Score 39.4; DB 4; Length 54; Pred. No. 7.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transposon; genetic engineering; transposase; Cat-Mu; ds.
                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 GAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 54
                                                                                                                                                                                                                                                                                                                                         Sequence 54 BP; 21 A; 12 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cat-Mu(NotI) transposon modified end fragment.
                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 7.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 2; Opp; English
                                                                         Claim 6; Col 2; 11pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACF58171 standard; DNA; 54 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-2003; 2003WO-FI000285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2002; 2002FI-00000746.
                                                                                                                                                                                                                                                                                                                                                                           ch 78.8%;
1 Similarity 97.6%;
40; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Savilahti H, Tieaho V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FINN-) FINNZYMES OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845329/78.
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage mu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003087370-A1
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by a transposase useful for producing deletion derivatives of polypeptide.

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frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of a transposon containing a genetically engineered translation stop signal sequence in three reading frames at least partly within a transposon end sequence recognized by a transposase; and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a modified Cat-Mu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic engineering; transposase; Cat-Mu; ds.
                                                                                                                                                                                                                                                                                                                                                                containing Mu ends with engineered NotI restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54 BP; 19 A; 14 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 78.8%; Score 39.4; DB 10 1 Similarity 97.6%; Pred. No. 7.5e-05; 40; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cat-Mu transposon containing wild-type Mu ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 2; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2002; 2002FI-00000746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-APR-2003; 2003WO-FI000285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACF58170 standard; DNA; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-845329/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage mu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003087370-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transposon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACF58170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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15 GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 55

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acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a \operatorname{Cat-Mu} transposon containing wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of detecting a mismatch in a test double stranded nucleic acid target which comprises detecting transposition of the Mu-end nucleic acid into the target, where transposition at the predominant site indicates the presence of mismatch at about that site. The methods are useful for typing a pathogenic microorganism strain, for screening an embryo for the presence of mutation, for detecting the presence of known mutation in a gene of interest, detecting the presence of known mutation in a gene of interest, and diagnosing the presence or absence of a tumour-promoting mutation. The kit is useful for detecting the presence of a mutation or polymorphism of interest in a nucleic acid molecule. The present sequence represents the Mu end DNA fragment construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a mismatch in a test double stranded nucleic acid target, useful for typing a pathogenic microorganism strain, comprises detecting transposition of the Mu-end nucleic acid into the target.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; mismatch detection; transposition detection; pathogen typing; embryo screening; mutation detection; Mu end DNA; MM1138.
                                                                                                                                                     ö
                                                                                                                Length 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 78.8%; Score 39.4; DB 13; Length 56; Best Local Similarity 97.6%; Pred. No. 7.6e-05; Matches 40; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mu end DNA fragment construction oligonucleotide MM1138.
                                                                                                                                                                                      10 GAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                         14 GCACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 54
                                                                           Sequence 54 BP; 21 A; 12 C; 14 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56 BP; 22 A; 12 C; 15 G; 7 T; 0 U; 0 Other;
                                                                                                              Score 39.4; DB 10;
Pred. No. 7.5e-05;
                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1; 24pp; English.
                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2004; 2004US-00809688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2003; 2003US-0457934P.
                                                                                                            Query Match
Best Local Similarity 97.6%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                    ADS13820 standard; DNA; 56
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizuuchi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterobacteria phage Mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSA ) US SEC OF ARMY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004191821-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yanagihara K,
                                      -type Mu ends
                                                                                                                                                                                                                                                                                                                                                                                             16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                 RESULT 9
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The invention relates to a Mu-like transposable element (I) used for generating functional fusion proteins after insertion into a target DNA. The Mu-like element comprises: (a) a left transposable element attachment and attR; (c) after insertion of the transposable element into a target DNA sequence, a fusion mRNA sequence is transcribed originating either from the target DNA on either side of the transposable element or from inside the transposable element and continuing through the attachment site sequences and into the protein coding region, resulting in a single fusion open reading frame (ORF). The constructs are useful in the development of a protein domain library, in the construction of multicunctional enzymes and in the accelerated evolution of new enzymatic activities. The sequences AAZ28804 represent deletion mini-Mu elements of the invention (encoded ORF - AAX55901-Y55906)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generating fusion proteins using transposable elements, useful for development of a protein domain library and in the construction of multifunctional enzymes.
                                                                                                                                                                                                                                              Transposon Mu; transposable element; fusion protein; attachment site; attL; attR; protein domain library; enzyme; accelerated evolution; ss.
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                                                                                                                                                                                       Mini-Mu transposable element deletion region delta-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaines GL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weber JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 2; 41pp; English.
   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casadaban MJ, Demirjian DC,
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AAZ28882 standard; cDNA; 71
AAZ28883 standard; cDNA; 58
                                                                                                                       15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DEMI/) DEMIRJIAN D C.
(CASA/) CASADABAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-633307/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GAIN/) GAINES G L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WEBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      USS981177-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999.
                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                             AAZ28883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CASA/)
(WEBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
AAZ28882/c
ID AAZ28
XX
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Gaps

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10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50

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deletion; plant genome; animal genome; primer; PCR; ss
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                                                WO2003031629-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5981177-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1999
                                                                         17-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ28881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ28881,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a Mu-like transposable element (I) used for generating functional fusion proteins after insertion into a target DNA. The Mu-like element comprises: (a) a left transposable element attachment attendent attachment attendent attachment attendent attachment attendent attachment attendent attachment attendent attachment and attra. (c) after insertion of the transposable element into a target DNA sequence, a fusion many sequence is transcribed originating either from the target DNA on either side of the transposable element or from into attachment site sequences and into the protein coding region, resulting in a single fusion open reading frame (ORF). The constructs are useful in the development of a protein domain library, in the construction of multicactional enzymes and in the accelerated evolution of multicactivities. The sequences AAZ28884 represent deletion mini-Mu elements of the invention (encoded ORF - AAY55901-Y55906)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                             Generating fusion proteins using transposable elements, useful for development of a protein domain library and in the construction of multifunctional enzymes.
                                                                         Transposon Mu; transposable element; fusion protein; attachment site; attL; attR; protein domain library; enzyme; accelerated evolution; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting construct; targeting vector; transposon; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.8%; Score 39.4; DB 2; Length 71; ilarity 97.6%; Pred. No. 7.8e-05; Conservative 0; Mismatches 1; Indels
                                                  Mini-Mu transposable element deletion region delta-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAAC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 71 BP; 14 A; 18 C; 16 G; 23 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                Gaines GL;
                                                                                                                                                                                                                                                                                                Weber JM,
                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Fig 2; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         踞.
                                                                                                                                                                                                                                                                                                Casadaban MJ, Demirjian DC,
                                                                                                                                                                                    95US-00378548
                                                                                                                                                                                                            95US-00378548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC80745 standard; DNA; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                          (first entry)
                                                                                                                                                                                                                                   DEMIRJIAN D C.
CASADABAN M J.
                                                                                                                                                                                                                                                                                                                        WPI; 1999-633307/54.
                                                                                                                                                                                                                                                                        (GAIN/) GAINES G L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                            WEBER J M.
                                                                                                                                                                                                            25-JAN-1995;
                                                                                                                                                                                    25-JAN-1995;
                           15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2003
                                                                                                                                      JS5981177-A.
                                                                                                                                                              .9-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC80745;
   AAZ28882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                              (CASA/)
(WEBE/)
                                                                                                                                                                                                                                    (DEMI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
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The invention relates to methods of preparing a targeting construct for use in a targeting vector capable of modifying a target DNA sequence, by obtaining a copy of the target DNA sequence in vitro, inserting a DNA sequence comprising a transposon sequence and a DNA recombination sequence comprising a transposon sequence and a DNA recombination sequence, and inducing a recombination event between the recombination sequences to delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target construct for use in a targeting vector for gene targeting or homologous recombination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
                                                                                                                                                                                                                                                                                                                                                               Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transposon Mu; transposable element; fusion protein; attachment site; attL; attR; protein domain library; enzyme; accelerated evolution; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mini-Mu transposable element deletion region delta-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 GAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 82 BP; 35 A; 21 C; 16 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
8e-05;
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.4; DB; Pred. No. 8e-050; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        and/or animal genome in a predetermined way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 51; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.8%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00378548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00378548.
                                                                 09-OCT-2001; 2001AU-00008174.
23-MAY-2002; 2002AU-00002522.
08-OCT-2002; 2002WO-AU001367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      881/c
AAZ28881 standard; cDNA; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.6'
Watches 40; Conservative
                                                                                                                                                                  (COPY-) COPYRAT PTY LTD
                                                                                                                                                                                                                                   Morrison J, Zhang C;
                                                                                                                                                                                                                                                                                                     WPI; 2003-393445/37.
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The invention relates to a Mu-like transposable element (I) used for generating functional fusion proteins after insertion into a target DNA. The Mu-like element comprises: (a) a left transposable element attachment site attL and a right transposable element attachment site attR, where attR is no more than 62 nucleotides long; (b) a site for insertion of an exogenous DNA sequence encoding for a protein domain located between attL and attR; (c) after insertion of the transposable element into a target DNA sequence, a fusion mRNA sequence is transcribed originating either from the target DNA on either side of the transposable element or from inside the transposable element and continuing through the attachment site sequences and into the protein coding region, resulting in a single fusion open reading frame (ORF). The constructs are useful in the development of a protein domain library, in the construction of multicunctional enzymes and in the accelerated evolution of new enzymatic activities. The sequences AAZZ8884 represent deletion mini-Mu elements of the invention (encoded ORF - AAYS5901-YSS906)
                                                                                                                                                                                              Generating fusion proteins using transposable elements, useful for development of a protein domain library and in the construction of multifunctional enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 83 BP; 17 A; 19 C; 18 G; 29 T; 0 U; 0 Other;
                                                                                                    Gaines GL;
                                                                                                    Weber JM,
                                                                                                                                                                                                                                                                                                Example 2; Fig 2; 41pp; English.
                                                                                                    Casadaban MJ, Demirjian DC,
(CASA/) CASADABAN M J.
(WEBE/) WEBER J M.
(GAIN/) GAINES G L.
                                                                                                                                                  WPI; 1999-633307/54.
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                                       Gaps
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0
ch 78.8%; Score 39.4; DB 2; Length 83; I Similarity 97.6%; Pred. No. 8e-05; 40; Conservative 0; Mismatches 1; Indels
                                                                      10 GAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                          GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 34
     Query Match
                       Local
                                    Matches
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Transposon-based targeting construct related primer Mul-4.
         ВЪ
         ACC80741 standard; DNA; 83
                           (first entry)
                                                                    WO2003031629-A1
                           15-OCT-2003
                                                  deletion;
                                             Targeting
                                                           Synthetic
                  ACC80741;
RESULT 14
ACC80741
```

construct; targeting vector; transposon; recombination; plant genome; animal genome; primer; PCR; ss.

17-APR-2003.

D8-OCT-2002; 2002WO-AU001367

09-OCT-2001; 2001AU-00008174. 23-MAY-2002; 2002AU-00002522.

(COPY-) COPYRAT PTY

Zhang Morrison J,

WPI; 2003-393445/37.

Preparing a targeting construct using a transposon and DNA recombination

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The invention relates to methods of preparing a targeting construct for use in a targeting vector capable of modifying a target DNA sequence, by obtaining a copy of the target DNA sequence in vitro, inserting a DNA sequence in vitro, inserting a DNA sequence comprising a transposon sequence and a DNA recombination sequence at two sites in the copy of the target DNA sequence, and inducing a recombination event between the recombination sequences to delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target construct for use in a targeting vector for gene targeting or homologous recombination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
sequence, useful in making a targeting vector capable of modifying plant and/or animal genome in a predetermined way.
                                                                                     Example 5; Page 50; 92pp; English.
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Gaps ö 1; Indels 10 GAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50 GCACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 64 8e-05; 0; Mismatches Score 39.4; Pred. No. 8e 78.8%; 97.6%; Conservative Local Similarity es 40; Conserv **datches** 셤 ઠે

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Length 83;

DB 10;

Sequence 83 BP; 29 A; 20 C; 18 G; 16 T; 0 U; 0 Other;

Query Match

Transposon-based targeting construct related primer Mul-1. ACC80738 standard; DNA; 84 (first entry) 15-OCT-2003 ACC80738; ACC80738

Targeting construct; targeting vector; transposon; recombination; deletion; plant genome; animal genome; primer; PCR; ss. 08-OCT-2002; 2002WO-AU001367 WO2003031629-A1 17-APR-2003. Synthetic,

(COPY-) COPYRAT PTY LTD Morrison J, Zhang C;

09-OCT-2001; 2001AU-00008174. 23-MAY-2002; 2002AU-00002522.

WPI; 2003-393445/37.

Preparing a targeting construct using a transposon and DNA recombination sequence, useful in making a targeting vector capable of modifying plant and/or animal genome in a predetermined way.

Example 5; Page 50; 92pp; English.

The invention relates to methods of preparing a targeting construct for use in a targeting vector capable of modifying a target DNA sequence, by obtaining a copy of the target DNA sequence in vitro, inserting a DNA sequence comprising a transposon sequence and a DNA recombination sequence at two sites in the copy of the target DNA sequence, and . inducing a recombination event between the recombination sequences to delete a portion of the copy of the target DNA sequence. The methods and compositions of the present invention are useful for preparing a target

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construct for use in a targeting vector for gene targeting or homologous recombination. They can also be used for precisely modifying plant and/or animal genome in a predetermined way. This sequence represents a primer used in an example of the invention
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Sequence 84 BP; 29 A; 20 C; 19 G; 16 T; 0 U; 0 Other;

ö; Gaps . 0 Query Match 78.8%; Score 39.4; DB 10; Length 84; Best Local Similarity 97.6%; Pred. No. 8e-05; Matches 40; Conservative 0; Mismatches 1; Indels 0

8 8

Search completed: January 17, 2006, 19:35:11 Job time : 32.092 secs

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OM nucleic

<u>6</u>

Run

Sequence:

Title:

Minimum DB 8 Maximum DB 8

Database

No.

Result

0 0 0

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Cryaz brachyantha

Eukaryotatha

Eukaryotatha

Eukaryothyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukartothyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae

I (bases 1 to 370)

Staim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,

Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

OMAP Project

L Unpublished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute
University of Arizona

Probes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 621 1259
                                                                                                                                                                                                                                                                                                                  GSS 20-JUN-2005
        CB222852 UCRCSUL
BI567751 BB170007B
BQ149276 NF088G08F
F05165 HSCO2H021 n
AA41614 aa35509.r
C14413 C14524 C10n
AA262843 2824405.r
C14413 C14413 C10n
AA994984 BT3167054
AC998995 RPCI-23-2
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AL041260 DKFZP434L
CF449523 EST6868
BI93390 HYSMEMBOOI
BI772228 603056184
BR948532 BST114366
BR964853 AGENCOURT
AZ176111 SP 0140 B
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BM085322 BW085322
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/dev_stage="mature"
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                                                                                                                                                                                                                               CR792741 GR0AAA1BE
                                                                                                                                                                                                                                                                                                                CZS69838 370 bp DNA linear GS6
OB Ba0003F02.r OB Ba Oryza brachyantha genomic clone
OB Ba0003F02 3', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwingegenome.arizona.edu
PCR PRiners
PCNMARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145 Std Brror: 0.00
Plate: 0003 row: F column: 02
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza brachyantha"
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                   BIS07751
BQ149276
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BI772228
                                                                                                                                                                DR952125
BM804853
AZ176111
BZ833089
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                                                                                                                                                                                                                                                                                                                                                         CZ569838.1 GI:68013639
                                                                                                                                                                                                                                                                                                                                                                             Oryza brachyantha
1. .370
GSS
                             source
                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                            RESULT 1
CZ569838
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
ORIGIN
                                           0 0 0 0 0 0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C2569838 OB BB000
CC742071 ZMMBBb011
CL858345 OR CB008
CZ821413 OC B019
CZ820900 OC B019
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B1953982 HVSMEm001
B1953934 HVSMEm001
B1953957 HVSMEm001
B1953931 HVSMEm001
B1953902 HVSMEm001
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AZ152875 SP 0046 B
CN586362 USDA-FP 1
T31184 EST28439 Hu
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DN797614 USDA-FP/A
BI954000 HVSMEm001
BI953998 HVSMEm001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CZ821171 OC Ba019
BJ016030 BJ016030
                                                                  January 17, 2006, 18:09:28; Search time 211.625 Seconds (without alignments) 11054.239 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                 1 tgattgattgaacgaaaaac......ttcacgataaatgcgaaaac
                                                                                                                                                                                                          82156650
      GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
                                                                                                                                                                                    41078325 segs, 23393541228 residues
                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                nucleic search, using sw model
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CZ821413
CZ820900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CZ821171
BJ016030
DU032104
BI953982
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BI953957
BI953931
BI953878
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CF504687
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BI954000
BI953998
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seq length: 200000000
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Match Length DB
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gb_est2:*
gb_htc:*
gb_est4:*
gb_est5:*
gb_est6:*
gb_est5:*
gb_est6:*
gb_est6:*
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                                                                                                                                                                                                                                                                                                      EST: *
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CC742071

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TITLE JOURNAL COMMENT

REFERENCE AUTHORS

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543 bp DNA linear GSS 26-JUL-2005 OC Ba0199Pl3.r OC Ba Oryza coarctata genomic clone OC Ba0199Pl3 3', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="young leaves"
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/lone lab-ioR CBa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza coarctata (Porteresia coarctata)
Oryza coarctata
Dukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
I (Basea I to S43)
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,
Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryza.

1 (bases 1 to 589)

Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Bullding Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 78.8%; Score 39.4; DB 10; Length 589; 1 Similarity 97.6%; Pred. No. 0.00054; 40; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                OMAP project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Porbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 622 9595
Pax: 520 621 1259
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0089 row: D column: 12
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. :589
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PCR PRimers
FORWARD: TAA TAC GAC TCA CTA TAG GG
                                                                                                                                                                                                                                                                                                                               Email: rwing@genome.arizona.edu
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Best Local Similarity
Matches 40; Conserva
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AUTHORS
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KEYWORDS
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CZ821413
LOCUS
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CL858345 CL858345.1 GI:S1269584
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                                                                                                                                                                                                                                              CC742071 226 bp DNA linear GSS 25-JUN-2003
ZMMBBb0115J07.£ ZMMBBb Zea mays genomic clone ZMMBBb0115J07 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 226)
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J. and Wing, R.
                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="ZMMBBb"
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HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Augurating of the maize genome
Unpublished (2003)
Contact: Rood Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
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                                                   0;
    Score 40.4; DB 10; Length 370;
Pred. No. 0.00023;
0; Mismatches 1; Indels 0
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                                                                                          / Match 78.8%; Score 39.4; DB 9; Local Similarity 97.6%; Pred. No. 0.00053; nes 40; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                           genomic survey sequence. CC742071
                                                                                                                                                                                                                                                                                                                                    CC742071.1 GI:32194524
         Query Match
Best Local Similarity 97.6%;
Matches 41; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ends.
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Oryza rufipogon
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CABAD199J21.r OC_Ba Oryza coarctata genomic clone OC_Ba0199J21.
3/, genomic survey sequence.
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BJ016030 MF01SSA CDNA Oryzlas latipes CDNA clone MF01SSA008A02 3',
mRNA sequence.
BJ016030
                                                                                                                                                                                                                                                                                                                                                               Oryza coarctata
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Li (basea I to 24, Wissotski, M., Byrne, M., Stum, D., Smart, D.,
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,
M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryzias latipes (Japanese medaka)
Oryzias latipes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Oryza Map Alignment Project) - Arizona Genomics Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
Arizona Bullding Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fex: 520 621 1259
    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
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                                              10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .247
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    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR PRIMERS
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0199 row: J column: 21
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ016030.1 GI:17375178
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    38; Conservative
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OMAP (O
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KEYWORDS
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JOURNAL
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    Matches
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CZ821171
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BJ016030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CZ820900
OC_Ba0199D21.r OC_Ba Oryza coarctata genomic clone OC_Ba0199D21
3', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryotas, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Voales; Voaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 688)
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute Unpublished (2005)
Contact: Rod A. Wing Ar Arizona Genomics Institute Arizona Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.4%; Score 36.2; DB 10; Length 543; Best Local Similarity 92.7%; Pred. No. 0.0083; Matches 38; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.2; DB 10; Length 688; Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Arizona
Forbes Bullding Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 GCACGAAAATGCGAAAGCGTTTCACGATACATGCGAAAAC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza coarctata (Porteresia coarctata)
Oryza coarctata
                                                                                                          1. .543
/organism="Oryza coarctata"
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0199 row: D column: 21
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0199 row: P column: 13
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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1. 688
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CZ820900
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Elycopersicon esculentum

Elycopersicon esculentum

Elycopersicon esculentum

Elycopersicon esculentum

Elycopersicon esculentum

Elycopersicon esculentum

Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

Elycopersicon.

Sweller, L.A., Buelas, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,

Van Eck, J. and Stack, S.

BAC end sequencing from three Solanum lycopersicon libraries

Unpublished (2005)

Other GSSs: 13518

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Cornell University

Z51 Emerson Hall, Ithaca, NY 14853, USA

Tel: 607-255-6683

Email: Sgn-feedback@sgn.cornell.edu
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                                     L (bases 1 to 582)

Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab
Unpublished (2001)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Mishima, Shizuoka 411-8540, Japan
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-685
Fax: 81-559-81-685
Email: tshini@genes.nig.ac.jp.
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13515 Tomato HindIII BAC Library Lycopersicon esculentum genomic clone LE_HBa0169A20 3, genomic survey sequence.
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Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGATTGATTGAACGAAAAACGCGAAAGCGTTTCACGATAAATGCGAAAA 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.2%; Score 26.6; DB 3; Length 582; 71.4%; Pred. No. 30; ive 0; Mismatches 14; Indels
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/mol type="genomic DNA"
/culfivar="Heinz 1706"
/db xref="taxon:4081"
/clone="LE_HBa0169A20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="segmentation_stage 20
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                                                                                                                                                                                                                                                                                                                                                                                                         (db_xref="taxon:8090"
|Clone="WRD1SSA008A02"
|sex="mixture of female and male"
|tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                          'organism="Oryzias latipes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 36
High quality sequence stop: 428.
Location/Qualifiers
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Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="Hd-rR"
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Best Local Similarity 71.4
Matches 35; Conservative
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/ Jone libe-Hordeum vulgare green seedling EST library HVCDNA0014 (Blumeria infected)"

HVCDNA0014 (Blumeria infected)"

Anotes-Weetor: pBluescript SK(-); Site_1: ECORI; Site_2: Morex (mla) plants were greenhouse grown in the R Wise lab at lows State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammins f. sp. hordei, and leaves were harvested Blumeria grammins f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA plagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 19-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HVSMEm0015K12f Hordeum vulgare green seedling EST 19-OCT-2001 HVcDNA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA clone HVSMEm0015K12f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 215)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Oates,R. and Main,D.
Development of a generically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                693 GATGAATTAAAAGAAAAAAGAAGCAAGATTTTCACTAAATATGAGAAAAC 645
                                                                                                                                                                                                                                                                  2 GATTGATTGAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAAAC 50
                                                                                                                                  DB 10; Length 802;
/clone lib="Tomato HindIII BAC Library"
/note="Vector: pBeloBAC11; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare subsp. vulgare"
|mol_type="mRNA"
|cultivar="Morex"
                                                                                                                                                                                                    Indels
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/lab_host="TJC121"
                                                                                                                                                                                                 14;
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100 Jordan Hall, Clemson, SC 29634, USA
110 1864 656 7288
Pax: 864 656 4293
                                                                                                                               ; Score 26.6; DB
; Pred. No. 30;
0; Mismatches
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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Total hq bases = 174
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
High quality sequence stop: 216
Location/Qualifiers
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|db xref="taxon:112509"
|clone="HVSMEm0015K12f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI953982.1 GI:16299103
                                                                                                                                  ch 53.2%;
1 Similarity 71.4%;
35; Conservative
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Unpublished (2001)
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HVSMEm0015G22f Hordeum vulgare green seedling EST 19-OCT-2001
HVCDMA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA
B1953934
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Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Morex (mla) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                 above. For more details on library preparation and
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                                                                                                                                                                                                                                                                                                                                        52.4%; Score 26.2; DB 3; Length 215; 79.5%; Pred. No. 41; ive 0; Mismatches 8; Indels (
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/organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                               10 GAACGAAAACGCGAAAGCGTTTCACGATAAATGCGAAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 GCACGAAAACGCGAAAGCGTTGCACGTAAAAGCGAAAA 2
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/lab_host="TJC121"
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Clemson University Genomics Institute
Clemson University
LOG Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: AATTAACCTCACTAAAGGG
High quality sequence start: 25
High quality sequence scop: 736.
Location/Qualifiers
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/db_xref="taxon:112509"
/clone="HVSMEm0015G22f"
                                                                                                                                     sequence analysis see
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/cultivar="Morex"
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Unpublished (2001)
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BI953934/c
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Blumeria graminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo exclised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Sperarophyta; Magnoliophyta; Erilopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
I (bases I to 757)
I (bases I
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HVCDNA0014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEm0015112f, mRNA sequence.
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/organism="Hordeum vulgare subsp. vulgare"
/mol type="mRNA"
/culTivar="Morex"
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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; Pred. No. 42;
0; Mismatches
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Total hq bases = 590
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
High quality sequence stop: 756.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence analysis see
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Unpublished (2001)
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BI953957/c
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/sub_species="vulgare"

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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 6
High quality sequence stop: 197.
                                                                                                                                                                                                                                     /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEm0015G18f"
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                                                                                                       Location/Qualifiers
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87.5%;
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Total hq bases
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Best Local Simi
Matches 28;
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                                                                                                          FEATURES
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                                                                                            /lone lib="Hordeuw vulgare green seedling EST library //lone lib="Hordeuw vulgare green seedling EST library HVCDNA0014 (Blumeria infected)"
//note="Vector: pBluescript SK(-); Site_1: ECORI; Site_2: Xhof; Morex (mla) plants were greenhouse grown in the R Wise lab at lowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammins f: sp. hordei, and leaves were harvested grammins f: sp. hordei, and leaves were harvested lin the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA plagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Ming). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing) Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases I to 196)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Prisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
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HVCDMAD014 (Blumeria infected) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEm0015G18f, mRNA sequence.
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Pred. No. 60;
0; Mismatches 2; Indels 1
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                                                     /tissue_type="green seedling leaf"
/lab_host="TJC121"
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
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BI953931.1 GI:16299011
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Best Local Similarity 92.7'
Matches 38; Conservative
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/loo hose="locklaim" vulgare green seedling EST library //loo hose="locklaim" vulgare green seedling EST library HVCDNAOO14 (Blumeria infected)"
//note="Wector: pBluescript SK(-); Site_1: ECORI; Site_2: Khoi; Morex (mla) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IS; 7 day old green seedlings were infected with isolate 5874 of Blumeria grammins f. sp. hordei, and leaves were harvested Blumeria grammins f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-incoulation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pooldeae; Triticeae; Hordeum.

1 (bases 1 to 752)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Oates,R. and Main,D.
Development of a genetically and physically anchored BST resource
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/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
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                                                                                                                                                                                                                                                        /tissue_type="green seedling leaf"
/lab_host="TJC121"
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; Pred. No. 69;
0; Mismatches
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JOURNAL

source

FEATURES

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/done lib="Hordeur vulgare green seedling EST library //lone lib="Hordeur vulgare green seedling EST library HVcDNAG014 (Blumeria infected)"
//note="Vector: pBluescript SK(-); Site_1: BCORI; Site_2: Xho1; Morex (mla) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were infected with isolate 5874 of Blumeria gramminis f. sp. hordei, and leaves were harvested 24, 48 and 72 hr post-inoculation and snap frozen (Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Akkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Enlopsida; Poales; Poaceae;
Pooideae; Triticaee; Hordeum.

Ming, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T.,
Simmons, J., Oates, R. and Main, D.
Bevelopment of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected Morex (compatible) seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="green seedling leaf"
/lab host="TJC121"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
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87.5%; Pred. No. 71;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 16
High quality sequence stop: 619.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sub_species="vulgare"
/db_xref="taxon:112509"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Total hq bases = 486
                                                                                                                                                                                                                                                                                                                                                                               cDNA library
Unpublished (2001)
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Best Local Similarity
Matches 28; Conserv
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   for barley genomics: Blumeria infected Morex (compatible) seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="green seedling leaf"
/lab_host="TJC121"
                                                                                                                  Clemson University Genomics Institute
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Pax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                      Total hg bases = 537
Seg primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 15
High quality sequence stop: 729.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:112509"
'clone="HVSMEm0015C18f"
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cultivar="Morex"
                                                                                                                                                                                                                                                                                                          rwing@clemson.edu
                                      CDNA library
Unpublished (2001)
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                                                                                                        Contact: Wing RA
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Gaps

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Indels

BI953902/c DEFINITION

Matches

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ORIGIN

ACCESSION VERSION KEYWORDS

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GSS.

Lycopersicon esculentum (Solanum lycopersicum)

Lycopersicon esculentum

Eukaryoca, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryoca; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

Is (bases 1 to 973)

Wueller, L.A., Buels, R.M., Wang, Y., Tanksley, S.D., Glovannoni, J.J.,

Van Eck, J. and Stack, S.

BAC end sequencing from three Solanum lycopersicon libraries

Unpublished (2005)

Other GSSs: 24048

Contact: Lukas Mueller

Tanksley Lab, Dept. of Plant Breeding

Cornell University

Z51 Emerson Hall, Ithaca, NY 14853, USA

Tel: 607-255-6683

Email: sgn-feedback@sgn.cornell.edu

Plate: 44 row: G column: 12

Seq primer: SP6

Class: BAC ends

High quality sequence start: 50

High quality sequence stop: 416.
                                            DU005263 973 bp DNA linear GSS 12-AUG-2005 310893 Tomato Mbol BAC Library Lycoperation esculentum genomic clone SL Mbol0044G12 3, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="genomic DNA"
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/db xref="taxon:4081"
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/lab host="E. coli"
/clone lib="Tomato Mbol BAC Library"
/note="Vector: pBeloBAC11; Site_1: Mbol"

    .973
    /organism="Lycopersicon esculentum"

                                                                                                                                            DU005263.1 GI:72402335 GSS.
RESULT 15
DU005263
LOCUS
DEFINITION
                                                                                                                                                                                                                 ORGANISM
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VERSION
KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
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Search completed: January 18, 2006, 11:40:50 Job time : 212.625 secs

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AY744150 Dengue vi
AY65170 Dengue vi
AY244148 Dengue vi
AX243469 Chiheric
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AX243460 Chiheric
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                    5883141 seqs, 28421725653 residues
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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ACSOSS CLONING Vec ALGS9224 Plasmid p AY043299 Aeromonas D45834 Size marker L09155 pwT571 expr AX084356 Sequence U03501 Yeast replis U03499 Yeast episo U03499 Yeast episo AX093430 Allelic e AX093430 Allelic e AX093429 Allelic e AX093429 Allelic e AX093430 Allelic e AX093429 Allelic e AX08085 pmTNF-MPH p A7541 Sequence AR085100 Sequence AR209770 Sequence AR20976 Sequence AR3035 plasmid pIG A20356 plasmid pIG A20356 plasmid pIG A20356 plasmid pIG A20356 Cloning vec A20356 ASQUENCE	circular SYN 03-DEC-2004 , complete sequence.	vectors. .A., Murphy,B.R. and l infectious cDNA clone of an	f Infectious Diseases, NIAID, Bethesda, MD 20892, USA	2 vector p2(delta30)" 2"	
5228 11 XXU25059 56167 3 AJ639924 111823 1 AY043299 111943 1 SYNDKF339 3779 11 SYNDWT571V 4840 6 AX084356 5817 11 YRP7 10067 11 YRP7 10067 11 YRP7 11 YRP7 11 YRP7 11 YRP7 11 YRP7 12 YRP7 13 YRP7 14 YRP7 15 YRP7 16 AX0844 1474 6 AZ8085 1474 6 AZ8085 1474 6 AZ8085 1474 6 AR287564 1474 6 AR287565 1474 6 AR085100 1474 6 AR085101 1475 11 AF129432 15281 1 AF129432 11 AF129432 11 AY796342	ALIGNMENTS 15129 bp DNA 156089726	s type 2 vector p2(delta30) nces; artificial sequences; to 15129) Ur., Hanson, C.T., Hanley, K.S. didates derived from a nove notype dengue virus type 2 fect. Dis. 4 (1), 39 (2004)	to 15129) Saion 01-62-2004) Laboratory of ive, Bldg 50, Room 6515, Be	15129 Cganism="Dengue virus type 30_type="other DNA" Train="Tonga/74" D_xref="taxon:301536" Ountry="Tonga" 2016	vitus cype 1060" y vector pBR 1470"
24,469 30.24 30.24 30.25 3	AY744149 Dengue virus † AY744149 AY744149.1 G	Dengue virus type other sequences; a other sequences; a l (bases I to 15:1 Blanck, J.E. Jr., H Whitehead, S.S. Vaccine candidates American genotype of the part of	15461822 2 (bases 1 Whitehead, S Direct Subm Submitted (50 South Dr		/ 6 / 1 / 1 / 3 C
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LEKTKKOLGLGNIATQOPESNIIDIDLAPASAMTLYANATTFTTPMLAHSIENSSVNV SLTAIANQATVLMGLGKGWPLSKMDIGVPLLAIGCYSQVNPTTLTAALLLLJVAHYAII GPGLQAKATREAQKRAAAGIMKNPTVOSTTVIDLDPIPYDPREKQLGQWMLJVLCVT QVLMMRTTWALCBALTLAFREYDENGENFWNTTIAVSMANIFRGSYLÄGGGLLFSIMKNTTSTRRGTGYTTGATCBETGEKWKSRLNALGKSEFQIYKKSGIQEVDRTLAKEGIKG GETDHHAVSRGSAKLRWFVERNLVTPEGKVVDLGCGRGGWSYYCGGLKNVREVKGIK GGPGHEBPIPMSTYGWNLNVLQSGVDVVFFVPEKCIKTK
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NVHYWTEQYKFQPESPSKLASAIQKAHEBGIOCHTSKYTTLENIMWKQITSELMHILSE
NVHYWTEQYTGDIKGHWQVGKRSLRSPTELSYSWKTWGKAKNLSTELHNQTFLIDGPE
TAECPNTRRANSLEVEDYGFGVFTTNIWLREKQDVFCDSKLMSAAIKDNRAVHADE
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EQTLTILIRTGLLVISGLFPVSIPITAAAMYLMEVKKQRAGVLMDVPSPPPVGKAELE
DGAYRIKQKGILGYSQIGAGVYKEGTFHTWMHVTRGAVLMHKGKRIEBSWADVKKDLI
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GSPIVDKGKKVGLYGGWGVYTRSGAVSAIAQTEKSIEDDNETEEDDIFRKRKLTINDL
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TGREIVDLMCHATFTKLLEPIRKDLSPIRVPNIJIINDEAHFTDPASIAARGYISTKVEMGEH
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RODIAACLERNGKRVIQLSRKTFDSBTVKTRTWDWDFVVTTD SEMGAANFKAERVIDP
RRCMKPVILTDGEERVILAGEMPVTHSSAAQRRGRIGRNPRUENDGYYIWGEDENDE
DCAHWREAKMILLDNINTPEGIIPSLFFERENDAIDGEYRLRGEARKTFVDLMRRGD
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IYSDPLALKEFKEFAAGRKSLTLNLITEMGRLPTFWTQKARDALDNLAVLHTAEAGGK
AYNHALSELPETLETLLLTTLLATVTGGIFLFLMSGRGMGKWTLGMCCIITASILLWY
AQIQPHWIAASIILEFFLIVLLIPEPEKQRTFQDNOLTYVIIAILTVVAATWANEMGF
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SNASGNI.VSSVNMI.SRMI.NRPTMRHKKATYEPDVDLGSGTRNIGIESETPNLDI.IGK
RIEKIKQEHETSWHYDQDHPYKTWAYHGSYETKQTGSASSMVNGVVRLLTKPWDVVPM
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REBEPTKKVESNAALGAIFTDENKWKSAREAVEDSRFWELVDKBENLHLEGKCEFVYN
MMGKREKKLGEPGKAKGSRAIWYMLGARFLEFEALGFLNEDHWFSRENSLSGYBGEG
LHKLGYILREVSKKEGGAMYADDTAGWDTRITTEDLKNEEMITNHMAGEHKKLAEAIF
                                                                                                                                                                                                                                                                                                                                       IVTCAMFTCKKNMEGKIVQPENLEYTVVITPHSGEEHAVGNDTGKHGKEVKITPQSSI
TEAELTGYGTVTMECSPRTGLDFNEMVLLQMEDKAWLVHRQWFLDLPLPWLPGADTQG
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ETTMRGAKRMAILGDTAWDFGSLGGVPTSIGKALHQVFGAIYGAAFSGVSWTMKILIG
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NRPGYYTQTAGPWHLGKLEMDFDFCEGTTVVVTENCGNRGPSLRTTTASGKLI TEWCC
RSCTLPPLRYRGEDGCWYGMEIRPLKEKEENLVSSLVTAGHGQI DNFSLGILGMALFL
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LAPRRVRPTFAAGLLJRKLLMWTINTIGTULLSQSSETBETILBLTTSGQDAALGMWTLK
MVRNMEXYQLAVTINALILCYPRAVILLQNAWKVGCTILAVVSVGPLLTTSGQGKADWIP
LALTIKGLNPTAIFLTLSRTINKKRSWPLNEAIMAVGMVSILASSLLKNDIPMTGPLV
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                                                                                                                                                  DTITYKCPFLKQNEPEDIDCWCNSTSTWVTYGTCTTTGEHRREKRSVALVPHVGMGLE
                                                                                                                                                                                          TRTETWMSSEGAWKHAQRIETWILRHPGFTIMAAILAYTIGTTHFQRVLIFILLTAIA
                                                                                                                                                                                                                                                 PSMTMRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTMAKNKPTLDFELIKTEAKQPA
                                                                                                                                                                                                                                                                                         TLRKYCIEAKLTNTTTDSRCPTQGEPTLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGG
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                                                                                               GMIIMLTPTVMAFHLTTRNGEPHMIVSRQEKGKSLLFKTKDGTNMCTLMAMDLGELCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      SNWIQKETLVTFKNPHAKKQDVVVLGSQEGAMHTALTGATEIQMSSGNLLFTGHLKCR
                                             KLFMALVAFLRFLTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLNILNRRRRTV
translation="mnnQrkkarnTPFnmLkrernrVSTVQQLTKRFSLGMLQGRGP1"
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product="membrane precursor protein (prM)"
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/product="envelope protein (E)"
/A22. .3477
/product="NS1 protein"
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'product="membrane protein (M)"
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11941
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                                                                                                                                                                                                                                                                                               Length 15129;
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                                                                                                                                                                                                                                                                                              DB 11;
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Pred. No. 0;
0; Mismatches
                                                                     6376. 6756
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6757. 6825
/product="2K protein"
6826. 7569
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15111. .15129
/note="SP6"
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7570. .10269
                                           /product="NS2B protein"
             product="NS2A protein"
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10650. .10658
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86.4%;
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Best Local Similarity 86.4
Matches 1943; Conservative
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nat_peptide
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4132 .4521 /product="NS2B protein" 4522 .6375 /product="N33 protein" 6376 .6756

product="NS2A protein"

nat_peptide

mat_peptide

mat_peptide mat_peptide

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RSCTLPPLRYRGEDGGWYGMEIRPLKKERENIVSSLVTAGHQIDNFSLGILGMALFL
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LAAFRVRPTFAAGLLLRKLTSKELMWTTIGIVLLSQSSIPETILELTDALALGMWVUK
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ALTIKGLIPUPPAIFIKTRIKKKSPRPLNBA AMVGHVSILASSLIGANIPIMTOIPMOPPAIFIKTRIKKKSPRPLNBA AMVGHVSILASSLIGANIPIMTOIPMOPPAIFIKNIPMOPPAIFIKNUSPREQUILTILIRTGLLIVISGLFPVSIPITAAAWYLWEVKKQRAGVLWDVPSPPPVGKAELE
BQTLTILIRTGLLIVISGLFPVSIPITAAAWYLWEVKKQRAGVLWDVPSPPPVGKAELE
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SYGGWKLEGEWKEGENEVQVLALEPGRNPRAVQTKPGALTRYNYGTIGAVSLDFSPGTS
SYGGWKLEGEWKEGENEVQVLALEPGRNPRAVQTKPGALTRYNYGTIGAVSLDFSPGTS
SYGGWKLEGEWKEGENEVQVLALEPGRNPRAVQTKFGALTRYNYGTIGAVSLDFSPGTS
SYGGWKLEGEWKEGENEVQVLALEPGRNPAVOTKFGALTRYNYGTIGAVSLDFSPGTS
SYGGWKLEGEWKEGENEVQVLALEPGRNPAVOTKFGALTRYNYGTIGAVSLDFSPGTS
SYGGWKLEGEWKEGENEVQVLALEPGRNPAVOTKFGALTRYNYGTIGAVSLDFSPGTS
SYGGWKLEGEWKEGENEVQVLALEPGRNPAVOTKFGALTRYNYGTIGAVSLDFSPGTS
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AGIFWTATPPGSRDPFPQSNAPIMDEEREIPERSWNSGHEWVTDFKGKTVWFYPSIKT
RRDIAACLERNGKRYIQLSRKTPDSEYVKTRYNDWDFVVTDISEMGANFKAERVIDP
RCMFVILTDGEERVILAGMPVTHSSAAQRRGRIGRNPRNDNDYIYWGFPLENDE
DCAHWEAKVLLDNITYPEGIIPSLFPPEREKYDAIDGEYRLRGEARKTFVDLARRGD
LPVWLAYKVAAAGINYADRRWCFDGTRNNQILEENVEVEIWTKEGERKKLKFPRDAR
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AYNHALSELPETLETLLLTLLATVTGGIFLFIMSGKGMGKMTLGMCCIITASILLMY
AQIQPHWIAASIILEFFLIVLLIPEPEKQRTPQDNQLTYVIIAILTVVAATMANEMGF
LEKTKKDLGLGNIATQQPESNILDIDLRPASAWTLYAVATTFITPMLKHSIENSSVNV
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GPGLQAKATREAQKRAAAGIMKNPTVDGITVIDLDPIPYDPKFEKQLGGVMLLVLCVT
QVLMMRTTWALCEALTLATGPVSTLWEGNPGRFWNTTIAVSMANIFRGSYLAGAGLLF
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VLNLVENWLNNNTQFCVKVLNPYMPSVIERMETLQRKYGGALVRNPLSRNSTHEMYWV
SNASGNIVSSVNMISRMLINRFTMRHKKATYEPDVDLGSGTRNIGIESETPNLDIIGK
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VTQMAMTDTTPFGQQRVFKEKVDTRTQEPKEGTKKLMKITAEWIMKELGKKKTPRMCT
REEFTKKVRSNAALGAIFTDENKWKSAREAVEDSRFWELVDKERNLHLEGKCETCVYN
                                                     KLEMALVAFIRFLTI PPTAGI LKRWGTI KKSKA INVLRGFRKEI GRMLNI LNRRRRTV
GMI I MLTPTVMAFHILTTRNGEPHMI VSRQEKGKSLI FKTKDGTNMCTLMAMDLGELCE
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PSMTMRCIGISNRDFVEGVSGSWVDIVLEHGSCVTTWAKNKPTLDFELIKTEAKQPA
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I VTCAMFTCKKNMEGKI VQPENLEYTVVI TPHSGEEHA VGNDTGKHGKEVKI TPQSSI
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SWNIQKETLYOTRKNPHAKKRQDVVVLGSDEGAMTALTGATELDMSGNLLETGHHKCR
LRWDKLQLKGANSYSWOTGKFKLVKETAETQHGTIVIRVQYEGGGSPCKIPFEIMDLER
RHVLGRLITWNPIVTEKDSPVNIEAEPPFGDSYIIIGVEPGQLKLDWFKKGSSIGQMF
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NVHTWTEQYKFQPESPSKLASAIQKAHEEGICGIRSVTRLENLMWKQITSELNHILSE
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GETDHHAVSRGSAKLRMFVERNLVTPEGKVVDLGCGRGGWSYYCGGLKNVREVKGITK
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AGWSLRETACLGKSYAQMWSLMYFHRRDLRLAANAICSAVPSHWIPTSRTTWSIHASH
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translation="MNNQRKKARNTPFNMLKRERNRVSTVQQLTKRFSLGMLQGRGPI/
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(39. .936
product="membrane precursor protein (prM)"

137. .2421 'product="envelope protein (E)" 712. .936 'product="membrane protein (M)"

2422. .3477 /product="NS1 protein" 3478. .4131

77. .396 product="virion capsid protein (virC)"

mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide

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                                                                                                                                                       22; Indels 283; Gaps
                                                                                                                                    DB 11; Length 15129;
                                                                                                                                  Score 1636.8;
Pred. No. 0;
0; Mismatches
6757, .6825
/product="2K protein"
6826. .7569
/product="NS4B protein"
7570. .10269
                                                           /product="NS5 protein"
10684. .10692
/note="KpnI/Agel linker"
15111. .15129
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Best Local Similarity 86.4%;
Matches 1943; Conservative
                                                                                                      /note="SP6"
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                                     CTTCCTAATGCAGAGTCGCATAAGGAAGAGGAGCGTCGACCGATGCCCTTGAGAGCCTTCAA
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 /organism="Cloning vector pGEM-3"
/mol_type="cuther DNA"
/db_xref="taxon:90108"
95. .10287
/note="encodes polyprotein precursor once Spel linker sequence is removed prior to preparation of infectious transcripts corresponding to the viral genome"
2346. .2368
/note="Spel linker; required for stable replication in Escherichia coli"
10700. .10708
/note="Spel linker"
15127. .15145
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                                                                                                                                                     Score 1636.8;
Pred. No. 0;
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Klfmalvaflrfltlpptagilkrwgtikkskainvlrcffkkeigrminilnrrrtv
Gmiimltptvmafhlttrngephmivsrqekgksllfktkogtnmctlmamdlgelce
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Submitted (07-SEP-2004) Laboratory of Infectious Diseases, NIAID,
50 South Drive, Bldg 50, Room 6515, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine candidates derived from a novel infectious cDNA clone of
                                                                                                                        CTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTTCTGGAGAAAACTCAACGAG
                                                         TGGTCCCGCCGCATCATACCGCCAGTTGTTACCCTCACAACGTTCCAGTAACCGGGCA
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                                 13278 IGITCATCATCAGRAACCCGTATCGTGAGCATCCTCTCTCGTTTCATCGGTATCATTACC
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Blaney,J.E. Jr., Hanson,C.T., Hanley,K.A., Murphy,B.R. and
Whitehead,S.S.

    15159
/organism="Dengue virus type 2 vector p2"

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Dengue virus type 2 vector p2
other sequences; artificial sequences; vectors.
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/organism="Cloning vector pBR322"
/mol_type="other DNA"
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|strain="Tonga/74"
|db_xref="taxon:301535"
|country="Tonga"
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GGGLITVYCVITGRSADLERRATDVKNDOQABISGSSPILLSTTISEGSSPISKRBEB
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BQAYRIKQKGILGYSQIGAGVYKEGTFHTWMHVTRGAVLMHKGKRIEBSWADVKKDLI
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GSPYUDKKGKVWGYKONGVYTRSGAYVSAIAQTEKSIEDNPBIEDDIFRKRALTIMDL
HPGAGKTKRYLPRAIVREAIKRGLRLUSTRVALARMENEBALRGLPIRVQTPAIRAGH TGREIVDLMCKATFTWRLLSPIRVPNYNLIINDBAHFTDPASIAARGYISTRVBKGEA
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GNDIAACLRKGKTVWFVPSIKT
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RRCMKEVILTDGEBRVILAGPMPVTHSSAAQRRGRIGRNFRNBNDQYIYMGBPLENDB
LDVMLAYKVAABGINYADRBCIIPSLEPERBKVADAIOGEYRKGBARKTFVDLMRRGD
LDVMLAYKVAABGINYADRBWGFDGTRNNQILEBNYGVBIWTRGGBRKKTKPRUDAR
IYSDPLAALKEFREFARAGRKSLTLNLITEMGRLDFTPMTQKARDALDNLAVLHTBABGGR TLRKYCI EAKLTNTTTDSRCPTQGEPTLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGG I VTCAMFTCKKNMEGKI VQPENLBYTVVI TPHSGEEHAVGNDTGKHGKEVKI TPQSSI TEAELTGYGTVTWECSPRTGLDFNEMVLLQMEDKAMLVHRQWFLDLPLPWLPGADTQG VTQMAMTDTT PFGQQR V FKEKVDTRTQE PKEGTKKLMK I TAEMLWKELGKKKT PRMCT REEFTKKVRSNAALGA I FTDENKWKSAREA VEDSR FWELVDKERNLHLEGKCETCVYN MMGKREKKLGEFGKAKGSRA I WYMWLGAR FLEFEALGFLNEDHWFSRENSLSGVEGEG KLTYQNKVVRVQRPTPRGTVMDIISRRDQRGSGQVGTYGLNTFTNMEAQLIRQMEGEG IFKSIQHLTASEEIAVQDWLVRVGRERLSRMAISGDDCVVKPLDDRFARALTALNDMG AYNHALSELPETLETLLLTLLTATVTGGIFLFLMSGRGMGKMTLGMCCIITASILLWY RIEKIKQEHETSWHYDQDHPYKTWAYHGSYETKQTGSASSMVNGVVRLLTKPWDVVPM LHKLGYILREVSKKEGGAMYADDTAGWDTRITIEDLKNEEMITNHMAGEHKKLAEAIF KVRKDIQQWEPSRGWNDWTQVPFCSHHFHELIMKDGRTLVVPCRNQDELIGRARISQG AGWSLRETACLGKSYAQMWSLMYFHRRDLRLAANAICSAVPSHWIPTSRTTWSIHASH EWMTTEDMLTVWNRVWILENPWMEDKTPVESWEEIPYLGKREDQWCGSLIGLTSRATW AKNIQTAINQVRSLIGNEEYTDYMPSMKRFRREEEEAGVLW" 97. .438 /product="anchored capsid protein (anchC)"

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product="NS1 protein"

.3477 .4131

97. .396 /product="virion capsid protein (virC)"

mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide mat_peptide

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g &	11372 ACATTTCCCGAAAAGTGCCACCTGACGTCTAGGAAACCATTATTATCATGACATTAACC 11431 1289 TATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCTCATGTTTGACAGGT 1348	8 & 8	24 21
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oy op	1769 CTATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGGTCATGAGCGC 1828	s 음 5	12992 CAGAATGAATCACCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCG 13051
상 임	1829 TTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCGGGGACTGTTGGGCGCCATCTC 1888	S 옵	ACCTGAGCAACAACATGAATGGTCTTCGGTTTTCGTGTAAAGTCTGGAAACGCGG
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Dengue virus type 3 vector p3
Other sequences; artificial sequences; vectors.

1 (bases 1 to 1376)
Blaney,J.E. Jr., Hanson,C.T., Firestone,C.Y., Hanley,K.A.,
Murphy,B.R. and Whitehead,S.S.
Genetically modified, live attenuated dengue virus type 3 vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-JUN-2004) Laboratory of Infectious Diseases, NIAID,
50 South Drive, Bldg 50, Room 6515, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                 TGTGGAACACCTACATCTGTATTAACGAAGCGCTGGCATTGACCCTGAGTGATTTTTTCTC
                                                                                           CCCATGAACAGAAATCCCCCTTACACGGAGGGATCAGTGACCAAACAGGAAAAAACCGCC
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                                                   TGTTCATCATCAGTAACCCGTATCGTGAGCATCCTCTCTCGTTTCATCGGTATCATTACC

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    Craganisma-Dengue virus type 3 vector p3"
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    /db_xref="taxon:284999"

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/note="Sleman/78"
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/organism="Dengue virus ty
/org.type="other DNA"
/db_xref="taxon:11069"
/note="$\text{Anol} 78"
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/note="encodes polyprotein precursor once Spel linker sequence is removed prior to preparation of infectious transcripts corresponding to the viral genome" 2346. 2368  
/note="Spel linker; required for stable replication in Bscherichia coli"  
10731. .10739  
/note="KpnI/Agel linker"  
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Db 13189 TGTGGAACACCTACATCTGTATTAACGAAGCGCTGGCTTGACCCTGAGTGATTTTTCTC 13248 Qy 2806 TGTCCCGCCGCATCCATACCGCCAGTTTAACCTCCACACGTTCCAGTAACCGGCCA 2865 13249 TGTCCCGCCGCATCCATACCGCCAGTTTTTACCCTCACACGTTCCAGTAACCGGCCA 13308 Qy 2866 TGTTCATCATCATCACTAACCCCTATCGTTGTTTTCATCAGTTACCTCAGTTACC 2925 Db 13309 TGTTCATCATCAGTAACCCGTATCGTGAGCATCCTTCTCTTCATCAGTAACCGGCA 13308 Qy 2926 CCCATGAACAGAAATCCCCCTTACACGGAGCATCATTCAT	69 AY243469 TION Chimeric Dengue NON AY243469.1 GI:3 DS	SOURCE Chimeric Dengue virus vector p4 (Delta30)-D2-CME ORGANISM Chimeric Dengue virus vector p4 (Delta30)-D2-CME other sequences; artificial sequences; vectors. REFERENCE 1 (bases 1 to 15237) AUTHORS Whitehead, S.S., Hanley, K.A., Blaney, J.E. Jr., Gilmore, L.E., Blkins, W.R. and Murphy, B.R. TITLE Substitution of the structural genes of dengue virus type 4 with those of type 2 results in chimeric vaccine candidates which are	attenuated for mosquitoes, mice, and rhesus monkeys JOURNAL Vaccine 21 (27-28), 4307-4316 (2003) PUBMED 14505913 REFERENCE 2 (bases 1 to 15237) AUTHORS Whitehead, S. S. TITLE Direct Submission JOURNAL Submitted (24-FEB-2003) LID, NIAID, 50 South Dr., Room 6515,	Bethesda, MD 20892, USA FEATURES Location/Qualifiers 115237 / organism="Chimeric Dengue virus vector p4(Delta30)-D2-CME" //ml tyne="Gencomic DNA"	/db_xref="taxon:227158" /focus 1source 1sm="Dengue virus type 4"	47	/organ /mol_t /db_xr	Source 234"O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O.O	CDS 9710263 /codon_start=1	/product="polyprotein precursor" /protein id="AAP06555.1" /db_xref="G1:30026606"	/translation="WINDRKKARNTPFNMLKRERNRYSTVQQLTKRFSLGMLQSKGFLL KLFMALVAFTLRFLTIPPTAGILKRWGTIKKSKAINVLRGFRKEIGRMLNILNRRRRTA GMIIMLIPTVMAFHLLTRNGEPHMIVSRQEKGKSLLFKTEDGVNMCTLMAMDLGELCE
	Oy 2309 GCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCGGCGCATCGGGATGCC 2368 Db 12469 GCGAGGCTGGATGGCTTCCCCATTATGATTCTTCTCGCTTCCGGCGATCGGGATGCC 12528 Qy 2369 CGCGTTGCAGGCCATGCTGCCAGGCAGGTAGATGACCATCAGGGACAGGTTCAAGG 2428 Db 12529 CGCGTTGCAGGCCATGCTGCCAGGCAGGTAGATGACACCATCAGGGACAGGTTCAAGG 12588	2429 12589 2489	2549 CCTTGCCCCCCCGCGTTGCGTCCCGTGCAGCCGGGCCACCTCGAAT 12709 CCTTGTCTCCCCCCGCGTTGCGTCGGGGTCCATGGAGCCGGGCCACCTCGAAT 2609 GGAAGCCGGCGATCGCGTTGCGTTCACCGATCACGAGCCGGGCCAATCGAAT 2609 GGAAGCCGGCGCACCTCGCTAACGGATTCACCACCTCCAAGAATTGGAGCCAATCAAT	DD 12769 ĠĠĀĠĊĊĠĠĊĠĊĊĊĊĊĊĊŦĀĀĊĠĠŦŦĊĠĊĊĀĊŦĊĊĀĀĠĀĀŦŦĠĠĀĠĊĀĀŦĊĀŦŢĆ 12828 Qy 2669 TTGCGGAGAACTGTGAATGCGCAAACCAACCATTGGCAGAATACATGCGCTCGĠC 2728 Db 12829 TTGCGGAGAACTGTGAATGCGCAAACCAACCTTGGCAGAACATATCCATCGCGTCGĠC 12888	QY 2729 ATCTCCAGCAGCGCGAGGGGCGATCTCGGGAGGGATGGGGAGGAGGAGGAGGAGGAGGAGGGAG	Qy 2777 2776 Dh 1988 andamememememememememememememememememememe	2777	Db 13009 CAGAATGAATCACCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCG 13068 Qy 2777	Db 13069 ACCTGAGCAACAACAATGAATGGTCTTCGGTTTTCGTGAAAGTCTGGAAACGCGG 13128	QY 2777 2777 2777 2776 Dh 13129 AAGTCAGGCCGTGCACCATTATGTTCCGGATCGCATCGC	2777

TEAELTGYGTVTMECSPRTGLDFNEMVILQMENKAWLVHRQWFLDLFLFWLFGADTOG SWNIQKETLTVTFKNPHAKKQDVVVLGSQBGAMFTALTGATTELJMSGGULLFTGHLKCR LRWDKLQLKGMSYSWCTGKFKVVKETAETQHGTTVIRVQYEGGGSPCKIPFEINDLEK RHVLGRLITVNPIVTEKDSPVNIEAEPPFGBSYIIIGVBEGQLKLNWFKKGESTGQMF ETTWRGAKRWAILGDTAWDFGSLGGVFTSIGKALHQVFGAIYGAAFSGVSWYMKILIG VIITWIGMNSRNTSWAWTCIAVGGITLFLGFTVQADMGCVASWSGKELKCGŠGIFVVD NVHTWTEQYKRQPESPARLASAILNAHKDGVCGIRSTTRLENVMWKQITNELNYVLWE RSCTMPPLRFLGEDGCWYGMEIRPLSEKEENMVKSQVTAGQGTSETFSMGLLCLTLFV EECLRRRVTRKHMILVVVITLCAIILGGLTWMDLLRALIMLGDTWSGRIGGQIHLAIM AVFKMSPGYVLGVFLRKLTSRETALMVIGMAMTTVLSIPHDLMELIDGISLGLILLKI VTQEDNTQVGTLALSITFIRSTMPLVMAWRITMAVLEVVTLIPLCRTSCLQKQSHWVB ITALILGAQALPVYLMTLMKGASRRSWPLNBGIMAVGLVSLLGSALLKNDVPLACPMV AGGLLLAAYVMSGSSADLSLEKAANVQWDEMADITGSSPIIEVKQDEDGSF\$IRDVEB TNMITLLVKLALITVSGLYPLAIPVTMTLMYMWQVKTQRSGALMDVFSPAATKKAALS LGYILEEIDKKDGDLMYADDTAGWDTRITEDDLQNEELITEQMAPHHKILA¶AIFKLT YQKKVVKVLRPTRGAVMDIISKKDQRGSGGVGTYGLMTFTMWSVQLIRQM®VIT QDDMQNPKGLKERVEKWLKGCGVDLKLRMAISGDDCVVKPLDERFGTSLLFÅLDDMGKV RKDIPQWEPSKGWKWWQEVPCSHHFHKIPWDGRSLVVPCKNQDELIGRAÅLSGCAG WSLRETACLGKAXAQMWSLMYFHRRDLRLASMAICSAVPTEWFPTSRTTWSIHAHHQM GGHDLTVVAGDVKGVLTKGKRALTPPVSDLKYSWKTWGKAKI FTPEARNSTFLIDGPD
SECPDRERAANNSLEVDBYGFGHPTHYN WMKFRESSBVCDHELMSAALKDGKAYHAD
MGYWLESSKNQTWQTERASLIERASLIEWTCLWPKTHTLWGVLESQWLIPKSYAGPPSQHN
YRQGYATQTVGPWHLGKLEIDPGECPGTTVT1QBCDHKGPSLEYTTASGKLYTQWC IKHAVSRGSSKIRWIVERGMVKPÄGKVVDLGCGRGGWSYMATLKAVTEVKGYTKGGP
RHEED PMATYGWNLVALLASVDDYYKRPBQVDTLCDIGESSSNPTIEBEKTLKAVLK
WYEBED ISSKEBECIKTLANDYNGTVIEELEKLQRKHGGNLVRCPLSRNSTHEMYVSGA
SGNIVSSVNTTSKMLLMRFTTRHRKPYTEKOVDLGAGTRSVSTETEKPDMTIGRRLQ RLQEEHKETWHYDQENPYRTWAYHGSYEAPSTGSASSWVNGVVKLLTKPWDVIPMVTO WANTDTTPGQQRVRYKEKVOPKTUPGKEGTRWWTTANWMYTANAWALLGKKOPBLCTREE FLAKTKSTBAGLGAVGGATSASBAVNDSRFWELVDKERALHQEGKCESCYVNWMG KREKKLGEFGRAKGSRAIWYMMLGARPLEFEALGFLNEDHWFGRENSWGVEGEGELH TLRKYCIBAKLTNTTTESRCPTQGEPSLNEEQDKRFVCKHSMVDRGWGNGCGLFGKGG IVTCAMFTCKKNMEGKVVQPENLEYTIVITPHSGEEHAVGNDTGKHGKEIKITPQSSI MTTEDMLKVWNRVWIEDNPNMTDKTPVHSWEDIPYLGKREDLWCGSLIGLSSRATWAK NIHTAITQVRNLIGKEEYVDYMPVMKRYSAPSESEGVL

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product="membrane precursor protein"
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/product="anchored capsid protein"
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product="virion capsid protein"
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'note="M"
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/product="envelope protein"
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Pred. No. 0;
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                                                                       /product="NS2B protein"
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6376. .6756
/product="NS4A protein"
6757. .6825
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7561. .10260
/product="NS5 protein"
3478. .4131
/product="NS2A protein"
4132. .4521
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Best Local Similarity 86.4%;
Matches 1943; Conservative 0
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AY243467
Chimeric Dengue virus vector p4(Delta30)-D2-ME, complete sequence.
AY243467
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Chimeric Dengue virus vector p4(Delta30)-D2-ME
Chimeric Dengue virus vector p4(Delta30)-D2-ME
other sequences; artificial sequences; vectors.

1 (bases 1 to 15239)
Whitehead, S.S., Hanley, K.A., Blaney, J.E. Jr., Gilmore, L.E.,
Elkins, W.R. and Murphy, B.R.
Substitution of the structural genes of dengue virus type 4 with
those of type 2 results in chimeric vaccine candidates which are
attenuated for mosquitoes, mice, and rhesus monkeys
Vaccine 21 (27-28), 4307-4316 (2003)
                                                                        CCCATGAACAGAAATCCCCCTTACACGGAGGCATCAGTGACCAAACAGGAAAAAACCGCC
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Coganism="Chimeric Dengue virus vector /mol_type="genomic DNA"
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/organism="Dengue virus type
/mol_type="genomic DNA"
/db_xref="taxon:11070"
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Direct Submission

Buntted (24-FBB-2003) LID, NIAID,
Bethesda, MD 20892, USA
Location/Qualifiers
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/codon_start=1
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 CTTGCATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAACCTACTACTGGGCTG
                                                CTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCCTTCAA
                                                                              CCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCACTTATGACTGT
                                                                                                                         CTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGGGTCATTTTCGGCCGA
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RKTROPGFYZYOKTETTILDVDLRASAMTILYAVATTILTHEMLEHTIFRTSANLIAA
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11157 TGTTGAATACTCATACTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGT 11216
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                                                                                                                                                                                                                                                                                         DB 11; Length 15239;
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0; Mismatches
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4134. .4523
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Best Local Similarity 86.4%;
Matches 1943; Conservative C
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NDIANCIRKSGKKVIQUSRKTPDTEYPKTKLTDWDFVYTTDISEMGANFPAĞRYÜPPR
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VEPWLSSKPEFCIKVLNPYMPTVIEELEKLQRKHGGNLVRCPLSRNSTHEMÎWVSGAS
GNIVSSVNTTSKMLLNRFTTRHRKPTYEKDVDLGAGTRSVSTETEKPDMTIÎGRRLQR
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ISKVRSNAAIGAVFQEEQGWTSASEAVNDSRFWELVDKERALHQGGKCESCVYNMMGK
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                                                                                                                                                                                                                                                                                        VTCAKFSCSGKITGNLVQIBNLEYTVVVTVHNGJTHAVGNDTSNHGVTAMITPRSPSV
BVKLPDYGBLTLDCEPRSGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAGADTSBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVLMIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVASWSGKELKCGSGIFVVDN
VHTWTEQYKFQPESPARLASAILNAHKDGVCGIRSTTRLENVMWKQITNELNYVLWEG
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SLRETACLGKAYAQMWSLMYFHRRDLRLASMAI CSAVPTEWPPTSRTTWSIHAHHQWM
TTEDMLKVWNRVWI EDNPNMTDKTPVHSWEDI PYLGKREDLWGSSLIGLSSRATWAKN
                                                                                                                          IVTYKCPLLVNTEPEDIDCWCNLTSTWVMYGTCTQSGERRREKRSVALTPHSGMGLET
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product="membrane protein"
                                339. .2423
product="envelope protein"
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34.0%; Score 1636.8;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 1943; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             /note="KpnI/Agel linker"
14990. .15239
                                                                                                                                                                                                                                        /product="NS4A protein"
6759. .6827
                                                                                                                 3480. .4133
/product="NS2A protein"
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4524. .6377
                                                                                                                                                                                                                                                                                                         /product="NS4B protein"
7563, .10262
                                                                                                                                                                                                                                                                                                                                           /product="NS5 protein"
10619. .10627
                                                                               2424. .3479
/product="NS1 protein"
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6828. .7562
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="SP6 promoter"
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441. .938 /product="membrane precursor protein" /note="prM" 714. .938

mat_peptide

mat_peptide

.02. .398 product="virion capsid protein"

mat_peptide

'note="virC"

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CCCTGAGTGATTTTCTC 2805
                                                                                          CGTTCCAGTAACCGGGCA 2865
                                                                                                                  TTCATCGGTATCATTACC 2925
                                                                                                                                            TAAAGTCTGGAAACGCGG 13016
TGCTGCAAAACGTCTGCG 12956
                                                  GGATGCTGCTGCTACCC 13076
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ircular SYN 14-JAN-2005 -ME, complete sequence. virus type 3 vaccine , Hanley, K.A., -ME

tious Diseases, NIAID, 1, MD 20892, USA ector

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                                                                                           / Organism="Cloning vector pBR322"

/ mol_type="other DNA"

/ bxref="taxon:47470"

15007. 15256

/ organism="Cloning vector pGEM-3"

/ mol_type="other DNA"

/ hol_type="other DNA"

/ hote="taxon:9108"

/ note="encodes polyprotein precursor once XhoI linker sequence is removed prior to preparation of infectious transcripts corresponding to the viral genome"

/ note="XhoI linker; required for stable replication in Becherichia coli"

/ note="XhoI linker; required for stable replication in Becherichia coli"

/ note="XpoI / AgeI linker"

/ note="XpoI / AgeI linker"

/ note="XpoI / AgeI linker"
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86.4%; Pred. No. 0;
iive 0; Mismatches
                                      /organiam="Dengue virus ty
/mol_type="other DNA"
/db_xref="taxon:11070"
10645. 15006
/mol_type="other DNA"
/db_xref="taxon:11069"
/note="Sleman/78"
2363. 10635
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organism="Dengue virus type 2 (NGC-prototype)"
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               /mol_type="genomic DNA"
/db_xref="taxon:11065"
2344. .10647
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     12854 ATGATCGTGCTCCTGTCGTTGAGGACCCGGCTAGGCTGGCGGGGGTTGCCTTACTGGTTAG 12913
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1 (bases 1 to 15268)
Whitehead, S.S., Hanley, K.A., Blaney, J.E. Jr., Gilmore, L.E., Elkins, W.R. and Murphy, B.R.
Substitution of the structural genes of dengue virus type 4 with those of type 2 results in chimeric vaccine candidates which are attenuated for mosquitoes, mice, and rhesus monkeys
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Submitted (24-PEB-2003) LID, NIAID, 50 South Dr., Room 6515,
Bethesda, MD 20892, USA
Location/Qualifiers
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Whitehead, S.S.
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THYTLLVKALL ITVSGLY PLAI PVYTHTAY WYWDWY WYRQABALWD VEBBAATKKAALS
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GRAFILINGKGI YGGYGWYTKSGDYVSAI TQABRATGED VEYDDED FRKRLTIMDL
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HPQAGTTKR I LDS I YRKALKRILIA PTRKVAVABMEBALKGLP RYQTPAKKSET
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Chimeric Dengue virus vector p4-D2-ME, complete sequence.
AY243466
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Chimeric Dengue virus vector p4-D2-ME
Chimeric Dengue virus vector p4-D2-ME
other sequences; artificial sequences; vectors.

I (bases I to 15270)
Whitehead, S.S., Hanley, K.A., Blaney, J.E. Jr., Gilmore, L.E.,
Elkins, W.R. and Murphy, B.R.
Substitution of the structural genes of dengue virus type 4 with
those of type 2 results in chimeric vaccine candidates which are
attenuated for mosquitoes, mice, and rhesus monkeys
Vaccine 21 (27-28), 4307-4316 (2003)
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Submitted (24-PEB-2003) LID, NIAID, 50 South Dr., Room 6515,
Bethesda, MD 20892, USA
Location/Qualifiers
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EKTKTDFGFYQVKTETTILDVDLRPASAWTLÝAVÁTTILTPWLRHTIENTSANLSLAA
IANQAAVLMCLGKGWPLHRWDLGVPLLAMGCYSQVNPTTLTASLVMLLVHYAIIGPGL
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KIDT PÖWEPSKGWKUNGEVPECSHHFTAT BWCDGRSLVVPCRNODELLGRAR ISGOAGM
SLRETACLGKAYAQMWSLMY FHRRDLALASMAI CSAVPTEWPTSRTTWS I HAHHQWM
TTEDMLKVWRKWI EDNPNMTDKTPVHSWEDI PYLGKREDLWCGSLIGLSSRATWAKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SCTMPPLRFLGEDGCWYGMEIRPLSEKEERNWYKSOVTAGOGTSETFSMGLLCLTLFVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVLGRLITVNPIVTEKDSPVNIEAEPPFGDSYIIGVERGQLKLNWFKKGSSIGQMFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHTWTEQYKFQPESPARLASA1LNAHKDGVCG1RSTTRLENVMWKQ1TNELNYVLWEG
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ROGYATQTVGPWHLGKLEIDFGECPGTTVTIQEDCDHRGPSLRTTTASGKLVTQWCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TÄLIIGÄQALPVYLMTLAKGASRRSWPLNEGIMAVGLVSLLGSALLKNDVPLAGPMVA
GGLLLAAYVMSGSSADLSLEKAANVQWDEMADITGSSPIIEVKQDEDGSFSIRDVEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAHWTEAKWLLDNI YTPEGII PTLFGPEREKTQAI DGEFRLRGEQRKTFVELMRRGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTETWMSSEGAWKHAQRIETWILRHPQFTIMAAILAYTIGTTHFQRALIFILLTAVAP
SWTWRCIGISNRDFVEGVSGGSWVDIVLEHGSCVTTWAKNKPTLDFELIKTEAKQPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAELTGYGTVTMECSPRTGLDFNEMVLLQMENKAWLVHRQWFLDLPLPWLPGADTQGS
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                                                                                                           type 2 (NGC-prototype)"
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IHTAITOVRALIGKEEYVDYMFVKRYSAPSESEGVL" "product="anchored capsid protein" "note="anchor" "product="virion capsid protein" "product="virion capsid protein" "note="virc" "product="membrane precursor protein" "note="product="membrane precursor protein" "note="product="membrane protein" "note="product="membrane protein" "product="membrane protein"	mat_peptide 9392423 mat_peptide 939envelope protein" /note="E" mat_peptide 24243479 /product="NSI protein"	mat_peptide	/product="NS4A protein 67596827 /product="2K protein" 68287562		Query Match Best Local Similarity 86.4%; Pred. No. 0; Matches 1943; Conservative 0; Mismatches 22; Indels 283; Gaps 1;	OY 1109 TGTGGAACACCTACATCTGTATTAACGAGCATTATTGAAGCATTTATCAGGGTTATTGT 1168	OY 1169 CTCATGAGCGGATACATATTGAATGTATTTAGAAAATAAACAAATAGGGGTTCCGCGC 1228 	OY 1229 ACATTICCCGAAAAGIGCCACCTGACGICTAAGAAACCATTATTATCATGACATTAAČC 1288 	QY 1289 TATAAAAATAGGGGTATCACGAGGCCCTTTCGTCTTCAAGAATTCTCATGTTTGACAGCT 1348 DD 11368 TATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCTCATGTTTGACAGCT 11427	OY 1349 TATCATCGATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGC 1408 	QY 1409 ACCGTGTATGAAATCTAACGATGCGCTCATGGTCATCGTCGCCCCGCACCGTCACCCTGGATGC 1468 DD 11488 ACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGC 11547	Qy 1469 TGTAGGCATAGGCTTGGTTATGCCGGTACTGCGGGCCTCTTGCGGGATATCGTCCATTC 1528 Db 11548 TGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCGTCCATTC 11607	Qy 1529 CGACAGCATCGCCAGTCACTCATGGCGTGCTAGCGCTATATGCGTTGATGCAATTTCT 1588 Db 11608 CGACAGCATCGCCAGTCACTATGGCGTGCTGCTGCTGCTGCTGCTTGATGCGTTGATTCT 11667	Qy 1589 ATGCGCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGCCGCCCCAGTCCTGCTCGC 1648

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TALILGAQALPVYLMTLMKGASRRSWPLNEGIMAVGLVSLLGSALLKNDVPLAGPWVA
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NDIANCLRKSGKKVIQLSRKTFDTEYPKTKLTDWDFVVTTDISEMGANFRAGRVIDPR
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MRTTWAFCEVLTLATGPILTLWEGNPGRFWNTTIAVSTANIFRGSYLAGAGLAFSLIK
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TLLCLIPTVMAPSLSTRDGEPLMIVAKHBRGRPLLFKTTEGINKCTLIAMDLGEMCED
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VTCAKFSCSGKI TGNLVQI ENLEYTVVVTVHNGDTHAVGNDTSNHGVTAMI TPRSPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVKLPDYGELTLDCEPRÄGIDFNEMILMKMKKKTWLVHKQWFLDLPLPWTAGADTSEV
HWNYKERMVTFKVPHAKRQDVTVLGSQEGAMHSALAGATEVDSGDGNHMFAGHLKCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLWIGTNSRNTSMAMTCIAVGGITLFLGFTVQADMGCVASWSGKELKCGSGIFVVDN
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GHDLTVVAGDVKGVLTKGKRALTPPVSDLKYSWKTWGKAKIFTPEARNSTFLIDGPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECPNERRAWNSLEVEDYGFGMFTTNIWMKFREGSSEVCDHRLMSAAIKDQKAVHADM
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VPKMSPGYVLGVFLRKLISRETALMVIGMAMTTVLSIPHDLMELIDGISLGLILLKIV
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                                    (08-JUN-2004) Laboratory of Infectious Diseases, NIAID, prive, Bldg 50, Room 6515, Bethesda, MD 20892, USA
                                                                                                                                   /organism="Dengue virus type 4 vector p4"
/mol_type="other DNA"
/db_xref="taxon:283795"
/focus
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10659. .15020
/organism="Cloning vector pBR322"
/mol_type="cther DNA"
/dD_xref="taxon:47470"
/15021. .15270
/organism="Cloning vector pGEM-3"
/mol_tyne="cther DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pGEM-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="polyprotein precursor"
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/db_xref="GI:49781323"
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/mol_type="other DNA"
/db xref="taxon:11070"
/country="Dominica"
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/db_xref="taxon:90108"
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Direct Submace
Submitted (08-JUN-2004, -
50 South Drive, Bldg 50, Room 6
Location/Qualifiers
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                                                                                                                                                                                                                                                                           12928 CAGAATGAATCACCGATACGCGAAGCGAAAGGTGAAGCGACTGCTGCTGCAAAACGTCTGCG 12987
                                                                                                                                                                                                                                                                                                                                                                            12988 ACCTGAGCAACATGAATGGTCTTCGGTTTCCGTGTTTCGTAAAGTCTGGAAACGCGG 13047
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AY648301
                                                                 ATCTCCAGCAGCCGCACGCGCGCATCTCGGGCAGCGTTGGGTCCTGGCCACGGGTGCGC 12867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dengue virus type 4 vector p4
Dengue virus type 4 vector p4
Dengue virus type 4 vector p4
Other sequences; artificial sequences; vectors.

1 (Dases 1co 15270)
Durbin,A.P., Karron,R.A., Sun,W., Vaughn,D.W., Reynolds,M.J.,
Perreault,J.R., Thumar,B., Men,R., Lai,C.J., Elkins,W.R.,
Chancok,R.M., Murphy,B.R. and Whitehead,S.S.
Attenuation and immunogenicity in humans of a live dengue virus
type-4 vaccine candidate with a 30 nucleotide deletion in its
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Whitehead, S.S.
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/BPWLSSKPEFCIKVLNPYMPTVIEELEKLQRKHGGNLVRCPLSRNSTHEMYWVSGAS
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/product="membrane protein precursor"
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/product="anchored capsid protein"
/note="anchor"
102. .398
/product="virion capsid protein"
/note="virC"
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/product="envelope protein"
/note="E"
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/product="membrane protein"
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/product="NS5 protein"
10650. .10658
/note="Kpn1/AgeI linker"
15021. .15270
/note="SP6"
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/product="NS1 protein"
3480. .4133
/product="NS2A protein"
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Murphy, B.R. and Whitehead, S.S.
Genetically modified, live attenuated dengue virus type 3 vaccine
candidates
Am. J. Trop. Med. Hyg. 71 (6), 811-821 (2004)
                                                                                                                                NIAID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102. .10279
/note="encodes polyprotein precursor once XhoI linker sequence is removed prior to preparation of infectious transcripts corresponding to the viral genome"
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/note="XhoI linker; required for stable replication in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATAAAATTAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCTCATGTTTGACAGCT
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20892, USA
                                                                                                                                                                               /organism="Chimeric dengue virus vector p4-D3L-ME"
/mol_type="other DNA"
/db xref="taxon:284997"
/focus
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                                                                                                                 Direct Submission
Submitted (16-UTW-2004) Laboratory of Infectious
50 South Drive, Bldg 50, Room 6515, Bethesda, MD
Location/Qualifiers
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                                                                                                                                                                                                                                                                      /organism="Dengue virus type
/mol_type="other DNA"
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/nofe="Sleman/78"
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10676. .15037
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/mol type="other DNA"
/db xref="taxon:47470"
15038. 15287
/organism="cloning vector pt
/mol type="other DNA"
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86.4%; Pred. No. 0;
tive 0; Mismatches
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/note="Kpn1/Age1 linker"
15269. .15287
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                                          Am. J. Trop. Med. Hyg.
15642976
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Whitehead, S.S.
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                                                                         CCTTGTCTGCCTCCCCGCGTTGCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGAAT 2608
                                                                                                                                     TIGCGGAGAACIGIGAAIGCGCAAACCAACCCIIGGCAGAACAIAICCAICGCGICCGCC 2728
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Chimeric dengue virus vector p4-D3L-MB
Cher sequences; artificial sequences; vectors.
1 (bases 1 to 15287)
Blaney,J.E. Jr., Hanson,C.T., Firestone,C.Y., Hanley,K.A.,
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p4-D3L-ME,
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LOCUS
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EKKOKOTWNNSNIIONGKHYKKPHYHYIYIARNPYTIESYBNKIKRKLGNSSYAHVEI
LDYTKGSYSYTIHESKOAIARNKHIYDKKDIININDFDIDRYITLDESQKRELKNLLL
DIYDDYNLYNLYNTKDLMAFIRLRGAEFGILNTNDVKDIVSTNSSAFRLWFEGNYQCGYRA
SYAKVLDAETGEIK"
                                       faecalis; expression is dependent upon integration event to create in frame start codon"
10619. .11413
       note="alkaline phosphatase; derived from Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTAGCGCTATATGCGTTGATGCAATTTCTATGCGCACCCGTTCTCGGAGCACTGTCCGAC
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|transl_table=11
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|protein_id="AAK21832.1"
|db_xref="GI:13549403"
                                                                                                                                                                                                                                                                       /note="confers kanamycin-resistance"
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Pred. No. 0;
0; Mismatches
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complement(11817. .12515)
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/transl_table=11
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                                                                                                                                                   /gene="aphA3"
10619. .11413
/gene="aphA3"
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99.9%;
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/db_xref="di:1354939"
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YKI VGNI PYHLSTQIIKKVVVESHASDIYLIVEEGFYKRTLDIHRTLGLLLHTQVSIQ
QLLKLPAECFHPREYVNSVLIKLTRHTTDVPDKYWKLYTYFVSKWVNREYRQLFTKNQF
FHQAMKHAKVNNLSTVTYEQVLSIFNSYLLFNGRK"
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FFIMQLVGQVPAALMVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGE
KQAIIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
QLQGSLAALTSLTSITGPLIVTAIXAASASTWNGLAMIVGAALYLVCLPALRRGAWSR
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                                                                                                                                                                                                                                       Clancy, A., Lee, M.H., Jones, A.L. and Rubens, C.E. Construction and characterization of transposon Tuphoz for the identification of genes encoding exported proteins in Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee, M.H., Clancy, A., Jones, A.L., Nittayajarn, A. and Rubens, C.E. Direct Submission Submitted (19-MAR-2001) Infectious Disease, Children's Hospital and Regional Medical Center, 4800 Sand Point Way NE, Seattle, WA 98105, USA
Claiborne, A. and Rubens, C.B. Characterization of Enterococcus faecalis alkaline phosphatase and use in identifying Streptococcus agalactiae secreted proteins J. Bacteriol. 181 (18), 5790-5799 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="TnphoZ mutagenesis vector pMHL120"
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/db_xref="texxon:156762"
/lab_host="Streptococcus agalactiae"
/note="transposon TnphoZ delivery vehicle"
complement (4167. .4928)
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/transl_table=11
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/allele="phoz2"
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/product="connective tissue activating peptide /standard_name="CTAP-III"
/note="[Leu21]; CTAP-III[Leu21]; putative"
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/standard_name="Rho-dependent terminator"
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/note="leader sequence; putative"
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1. 6343
/organism="unidentified clonin/mol_type="genomic DNA"
/db_xref="texon:45196"
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SYNCLCTAPS
Expression cloning activating peptide
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                 ATCATGGCGACCACCCGCCCTCTGGATCCTCTACGCCGGACGCATCGTGGCCGCATCTCTCTGCCATCTGCCATCCTGCCATCCTCTACGCCGACGCATCGTGGATCCTCTACGCCGACGCATCGTGGCCGCATCCTCTACGCCGACGCATCGTGGCCGCATCCTCTACGCCGACGCATCGTGGCCGCATCCTCTACGCCGACGCATCGTGGCCGCATC
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7107 CTTGGCAGAACATATCCATCGCGTCGCCATCTCCAGCAGCCGCACGCGGGGGCGATCTCGG
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                                                                                                             ACCGGCGCCACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCACCGATGGGGAAGAT
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1405	AGGCACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCTCGGGACCGTCACCCTGG 1464
1465	AIGCIGIAGGCAIAGGCIIGGIIAIGCCGGIACIGCCGGCCCTCTIGCGGGAIAICGTCC 1524
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1765	GCGCCTATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGA 1824
1825	GCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGGGACTGTTGGGCGCCA 1884
1885	TCTCCTTGCATGCACCATTCCTTGCGGGGGGGGGGCTCAACGGCCTCAACCTACTACTGG 1944
1945	GCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCלT 2004
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2065	CTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGCACGCGCTCTCGGGTCATTTTCG 2124
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2185	TCTTGCACGCCCTCGCTCAAGCCTTCGTCACTGGTCCCGCCACCAAACGTTTCGGCGAAA 2244
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Search completed: January 18, 2006, 04:26:11 Job time : 24858 secs

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January 17, 2006, 17:02:23 ; Search time 2993.54 Seconds (without alignments) 10717.687 Million cell updates/sec
GenCore version 5.1.6
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                                                                                      OM nucleic
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1 ggtaccctgtgaatgcgcaa.......taagatgcttttctgtgact 4814 Gapop 10.0 , Gapext 1.0 US-10-511-327-7 IDENTITY NUC 4814 Perfect score: Scoring table: Sequence:

9993994 Total number of hits satisfying chosen parameters:

4996997 seqs, 3332346308 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 8 B Minimum Maximum M

geneseqn2003ds:* geneseqn2004as:* geneseqn2003cs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2005s:* geneseqn2004bs: geneseqn2003bs:* N_Geneseq_21:* : geneseqn1980s:* geneseqn1990s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	4814	100.0	4814	01	ACF58174	Acf58174 Modified
7	1636.8	34.0	15153	12	ADG93315	Adq93315 DEN3 (Sle
٣	1636.8	34.0	15159	12	ADG93313	Adq93313 DEN2 (Ton
4	1560.6	32.4	7311	14	AEA06371	Aea06371 Novel bac
C S	1477.2	30.7	5926	~	AAV32978	Aav32978 In7 donor
و ن	1477.2	30.7	5926	9	AAD45060	Aad45060 pEM delta
c 7	1476	30.7	5926	~	AAV32977	Aav32977 In7 donor
œ ن	1476	30.7	5926	ø	AAD45059	Aad45059 Transposo
٥ 0	1476	30.7	5926	12	ADG46817	Adq46817 Donor pla
c 10	1474	30.6	5926	12	ADG46818	Adg46818 pEM DNA (
11	1447.8	30.1	4840	4	AAF59457	Aaf59457 Npro-hGH
c 12	1446.8	30.1	3474	~	AAQ29146	Aaq29146 pmTNF-MPH
c 13	1446.8	30.1	3474	N	AAQ51546	Aag51546 Expressio
c 14	1446.8	30.1	3801	12	ADL72227	Adl72227 DNA seque
15	1446.8	30.1	4245	œ	ABZ70623	Abz70623 Plasmid p
c 16	1446.8	30.1	5201	12	ADL72228	Adl72228 DNA seque
17	1446.8	30.1	11184	12	ADP86274	Adp86274 Hepatitis
18	1446.8	30.1	11184	12	ADP86276	Adp86276 Hepatitis
19	1446.8	30.1	11184	12	ADP86277	Adp86277 Hepatitis

Adp86273 Hepatitis	4		ıΩ	æ		_			'n	7	m	Adi41414 BB7 nucle	0 rep		Aav59364 Hepatitis	Abk87286 Hepatitis	Aca62469 DNA encod		6	Adf44791 De novo s	Adf44790 De novo s	Aaq70219 Plasmid p	Aaf25570 Vector pS	Aav81319 Plasmid p	Aah74745 Nucleotid	
2 ADP86273	12 ADP86264	2 ADP86266		2 ADP86268	2 ADP86270	2 ADP86271	2 ADP86272	2 ADP86269	12 ADP86275	2 ADP86267	3 ADT77488	10 ADI41414	13 ADT77500	0 ADI41413	AAV59364	ABK87286	ACA62469	AAQ11083	12 ADL72229	10 ADF44791	0 ADF44790	AAQ70219	AAF25570	AAV81319	AAH74745	
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20	21	22	23	24	25	56	27	28		30	31	32	33	34	35	36	37	'n	c 39	40	41	c 42	c 43	44	45	

ALIGNMENTS

New transposon nucleic acid comprising a genetically engineered translation stop signal within a transposon end sequence recognized by a transposase useful for producing deletion derivatives of polypeptide. Transposon; genetic engineering; transposase; Cat-Mu; Tn7-Kan; ds. Modified Tn7-Kan(Stop)-transposon. ACF58174 standard; DNA; 4814 BP. 14-APR-2003; 2003WO-F1000285. 18-APR-2002; 2002FI-00000746. (first entry) Savilahti H, Tieaho V; (FINN-) FINNZYMES OY WPI; 2003-845329/78. WO2003087370-A1. 15-JAN-2004 23-OCT-2003. Synthetic. ACF58174; RESULT 1 ACF58174

The invention relates to a transposon nucleic acid comprising a genetically engineered translation stop signal in the three reading frames at least partly within a transposon end sequence recognized by a transposase. The transposon is useful for producing deletion derivatives of polypeptide coding nucleic acids. The method involves performing a transposition reaction in the presence of a target nucleic acid containing a polypeptide coding nucleic acid and in the presence of a transposon containing a genetically engineered translation stop signal Claim 7; Page 31-32; Opp; English.

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                                                                                                                                                                                                                                                                                                                                                                          sequence in three reading frames at least partly within a transposod e sequence recognized by a transposase, and recovering a target nucleic acid having the transposon incorporated in the protein coding nucleic acid. The present sequence represents a modified Tn7-Kan(Stop)-
                                                               CCAGCAGCCGCACGCGCGCATCTCGGGCAGCGTTGGGTCCTGGCCCACGGGTGCGCATGA
                                                                                          CAGCGCCCTGCACCATTATGTTCCGGATCTATGTCGGGTGCGGAGAAAGAGGTAATGAAA
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                                Seguence 4814 BP; 1214 A; 1206 C; 1137 G; 1257
                                         Query Match
100.0%; Score 4814;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4814; Conservative 0; Mismatches
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CCGGCGCCACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCACCGATGGGGAAGATC CCGGCGCCACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCACCGATGGGGAAGATC GTCGACCGATCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATA GAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCCACCTGACGTCTA TCTTCAAGAATTCTCATGTTTGACAGCTTATCATCGATAAGCTTTAATGCGGTAGTTTAT TCATCCTCGGCACCGTCACCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGTACTGC CGGGCCTCTTGCGGGATATCGTCCATTCCGACAGCATCGCCAGTCACTATGGCGTGCTGC TAGCGCTATATGCGTTGATGCAATTTCTATGCGCACCCGTTCTCGGAGCACTGTCCGACC gerrragecegececeagreeregerregerragerageagecaeraregaega TGGCCGGGGGGCGCCATCTCCTTGCATGCACCATTCCTTGCGGCGGCGGTGC GAGAGCTTAGTACGTTAGCCATGAGGCTTTAGTTCGTTAAACATGAGAGCTTAGTACGTT CTGCTGATCTTCGGATCTATGTCGGGTGCGGAGAAAGAGGTAATGAAATGGCATCCGGAT TTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATGAATGTATTA

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                       AAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCA
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23-DEC-2002; 2002US-0436500P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                     New tetravalent vaccine containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4, useful for preventing of disease in humans caused by dengue virus, or for inducing immune
                                                                                                                                                                                                                                                                tetravalent and containing a common nucleotide deletion in the 3' untravalent and containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4. The invention may be useful for the development of compounds with a virucide or immunostimulant activity or as a vaccine. The tetravalent vaccine is useful in the prevention of disease in humans caused by dengue virus. Unlike previous tetravalent vaccine, the new tetravalent vaccine is unique since they contain a common shared attenuating mutation which eliminates the possibility of generating a virulent wild type virus in a subject to be vaccinated since each component of the vaccine possesses the same deletal attenuating deletion mutation. The vaccine also is able to induce humoral and cellular responses against al of the (non-)structural proteins present in each dengue virus serotype. The present sequence is that of the DEN3 cDNA plasmid p3 which is related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11366 ACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 15153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15153 BP; 4434 A; 3440 C; 3943 G; 3336 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                        This invention relates to a novel immunogenic composition being
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             <u>ن</u>
             Blaney
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34.0%; Score 1636.8; DB 12
Best Local Similarity 86.4%; Pred. No. 3.1e-297;
Matches 1943; Conservative 0; Mismatches 22;
               Falgout
                                                                                                                                                                                                                      Disclosure; SEQ ID NO 48; 181pp; English
               Markoff L,
               BR,
                 Murphy
                                                                       WPI: 2004-022612/02.
                                                                                          P-PSDB; ADG93316
                 SS,
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This invention relates to a novel immunogenic composition being tetravalent and containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4. The invention may be untranslated region of dengue types 1, 2, 3, and 4. The invention may be immunostimulant activity or as a vaccine. The tetravalent vaccine is useful in the prevention of disease in humans caused by dengue virus. Unlike previous tetravalent vaccine, the new tetravalent vaccine is unique since they contain a common shared attenuating mutation which eliminates the possibility of generating a virulent wild type virus in a subject to be vaccinated since each component of the vaccine possesses to induce humoral and cellular responses against a lof the (non-structural proteins present in each dengue virus serotype. The present sequence is that of the DENZ CDNA plasmid P2 which is related to the
                                                                                                        New tetravalent vaccine containing a common nucleotide deletion in the 3' untranslated region of dengue types 1, 2, 3, and 4, useful for preventing of disease in humans caused by dengue virus, or for inducing immune
                                                                                                                                                                                                                              Disclosure; SEQ ID NO 46; 181pp; English
                                         WPI; 2004-022612/02.
P-PSDB; ADG93314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
Hanley K;
                                                                                                                                                                                     response
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Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;

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Query Best Match	Match Local	34.0%; Score 1636.8; DB 12; Length 15159; Similarity 86.4%; Pred. No. 3.1e-297; 3; Conservative 0; Mismatches 22; Indels 283; Gaps 1;
ò	1109	TGTGGAACACCTACATCTATAACGAAGCATTATTGAAGCATTTATCAGGGTTATTGT 1168
qq	11252	TGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTTATCAGGGTTATTGT 11311
ŏ	1169	CTCATGAGCGGATACATATTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGC 1228
ор	11312	CTCATGAGGGGGTACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGC 11371
δ	1229	ACATTICCCGGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATGATGACATTAAGC 1288
q ₀	11372	ACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATTATCATGACATTAAGC 11431
à	1289	TATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCTCATGTTTGACAGGT 1348
qq	11432	TATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAGAATTCTCATGTTTGACAGGCT 11491
λŏ	1349	TATCATCGATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGGC 1408
qq	11492	TATCATCGATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCTAACGCAGTCAGGC 11551
δ	1409	ACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGC 1468
QC	11552	ACCGIGIATIOAAATCTAACAATGCGCTCATCGTCATCCTCGGCACCGTCACCCTGGATGC 11611
ò	1469	TGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCGTCCATTC 1528
qq	11612	TGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCCTCTTGCGGGATATCGTCCATTC 11671
ò	1529	CGACAGCATCGCCAGTCACTATGGCGTGCTAGCGCTATATGCGTTGATGCAATTTCT 1588
qq	11672	CGACAGCATCGCCAGTCACTATGGCGTGCTGCTGCGCGCTATATGCGTTGATGCAATTTCT 11731
ò	1589	ATGCGCACCGTTCTCGGAGCACTGTCCGACGCTTTGGCCGCCGCCCACCCA
QQ	11732	ATGCGCACCGCTTCTCGGAGCACTGCCGACCGCTTTGGCCGCCCCCCGGTCCTGCTCGC 11791
ò	1649	TTCGCTACTTGGAGCCACTATCGACTACGCGATCATGGCGACCACCCCGTCCTGTGGAT 1708
qq	11792	

کی و	1709	CCTCTACGCCGGACGCATCGTGGCCGCATCACCGGCGCCACAGGTGCGGTTGCTGGCGC 1768
à	16	TATCGCCGCCGCCGCCGATCGCGCAAGATCCGGCCTCGCCACTTCGGGGTCATCAGGGC 182
qq	11912	CTATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGC 11971
8 8	1829	TIGITITOGGCGTGGGTATGGTGGCAGGCCCGTGGCCGGGGACTGTTGGGCGCCATCTC 1888
3 8	88	ACTGGGCTG 194
: 셤	03	CTTGCATGCACCATTCCTTGCGCGGCGGTGCTCAACGGCCTCAACCTACTACTACTGCGCTG 12091
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3 2		CCAGTCAGTCCTTCCGGTGGGGGGGGGTGAACTATCGTCGCCGCGCTTATGACTGT 2068
전 전	15	22
δ	2069	CTGGGTCATTTTCGGCGA 212
QQ	12212	<u>Argcaactcgtaggacaggrgccggcagcgr</u>
à	12	188
Dp	12272	CGCTTTCGCTGGAGCGCGAAGATGATCGGCCTGTCGCTTGCGGTATTCGGAATCTT 123
ολ	18	48
Op	12332	CACGCCCTCGCTCCAAGCCTTCGTCACTGGTCCCGCCACCAAACGTTTCGGCGAGAAGCA 123
δ	2249	0
QQ	12392	<u>zarrarceccescarsecceaceceacectescracerriecrescerrecea</u>
ò	2309	SGCATCGGGATGCC 236
DÞ	12452	sacacrarcadarace 125
λ̈́O	2369	3GACAGCTTCAAGG 2428
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ò	2489	2548
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ò	2609	GCCAATCAATTC 2668
Db	12752	cggcggcactcgctaacggattcaccactccaagaattggagccaatcaat
<i>λ</i> ο	2669	SCGGAGAACTGTGAATGCGCAAACCAACCCTTGGCAGAAGATATCCATCGCGTCCGCC 2728
οqα	12812	cggagaactgtgaatgcgcaaaccaaccttggcagaacatarccatcgcgtcggc 128
ģ	72	TTCCAGCAGCCCCACGCGCACCCCTCGGCCACCTTGGCTCCTGG277
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CTATATICGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New bacterial host cell comprising at least two copies of an amplification unit in its genome, useful for increased production of a protein with several copies of a gene of interest stably chromosomally
                                         CAGAATGAATCACCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCG
                                                                                                    TGGTCCCGCCGCATCCATACCGCCAGTTGTTTACCTCACAACGTTCCAGTAACCGGGCA
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This invention relates to a novel bacterial host cell comprising at least two copies of an amplification unit in its genome, where two or more amplified chromsomal copies of the gene of interest are produced. The amplification unit comprises at least one copy of a gene of interest and amplification unit comprises at least one copy of a gene of interest and expressible conditionally essential gene, where the conditionally comprises or transcribed from a heterologous promoter having an activity substantially lower than the endogenous promoter of the conditionally essential gene, and where the conditionally compressed in the conditionally essential gene, and where the conditionally compressed in the conditional would render the cell auxotrophic for at least one specific substance or unable to utilize one or more specific sole carbon source. The bacterial host cell is useful for producing of a protein having several copies of a gene of interest stably chromosomally integrated, without leaving antibiotic resistance marker genes in the strains. The present sequence is that of a plasmid DNA sequence which was used in the exemplification of the invention.
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Pred. No. 5.7e-283;
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Example; SEQ ID NO 7; 53pp; English.
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DNA sequencing; genetic analysis;

insertional mutagenesis; ss transposable element;

WO9837205-A1

Synthetic.

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The present sequence represents a Tn7 donor plasmid pEM delta. Transposon Tn7 encodes an ATP-utilising regulatory protein that contains a mutation that allows efficient and simple insertion of, and reduced target site specificity of, a transposable element derived from the transposon. The ATP-regulatory protein and compositions are used for the efficient, nonspecific and simple insertion of a transposon or transposable element into a DNA segment. This is useful in DNA sequencing, for genetic analysis by insertional mutagenesis, or for alteration of gene expression

encoding mutant ATP using proteins for insertion - which irandom, with reduced site specificity; for DNA sequencing

97US-00037955 98WO-US003353

20-FEB-1998; 27-AUG-1998

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Craig NL;

Disclosure, Fig 10C; 143pp; English.

and altering gene expression.

efficient and

Transposon(s)

WPI; 1998-467567/40.

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                       Sequence 5926 BP; 1476 A; 1473 C; 1463 G; 1514 T; 0 U; 0 Other;
                                                   2; Length 5926;
                                                                             Indels
                                                30.7%; Score 1477.2; DB 2;
llarity 93.4%; Pred. No. 2.4e-267;
Conservative 0; Mismatches 38;
insertion of a desired sequence
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                                                              Best Local Similarity
Matches 1594; Conserv
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donor plasmid; transposon; ATP-utilising regulatory protein;

In7 donor plasmid sequence.

entry)

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17-NOV-1998

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DNA; 5926

standard;

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant TnsC transposition regulatory protein for use in DNA sequencing, for genetic analysis, and alteration of gene expression by insertion of given genetic sequence, comprises an alanine to valine substitution.
                                                                                                                 CATCTATTTTGTCACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAG
                                 TTCCAAACTATTTTGTCATTTTTAATTTTTCGTATTAGCTTACGACGCTACACCCCAGTTCC
                                                                                   CATCTATTTTGTCACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAG
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kanamycin gene with SalI sites at the junctions. The backbone is pTRC99 (Pharmacia). Transposon Tn7 encodes an ATP-utilising regulatory protein that contains a mutation that allows efficient and simple insertion of, and reduced target site specificity of, a transposable element derived from the transposon. The ATP-regulatory protein and compositions are used for the efficient, non-specific and simple insertion of a transposon or transposable element into a DNA segment. This is useful in DNA sequencing, for genetic analysis by insertional mutagenesis, or for alteration of gene expression by insertion of a desired sequence
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                                                                                                                   Sequence 5926 BP; 1476 A; 1473 C; 1463 G; 1514 T; 0 U; 0 Other;
                                                                                                                                        Query Match 30.7%; Score 1476; DB 2; Length 5926; Best Local Similarity 93.6%; Pred. No. 4.1e-267; Matches 1591; Conservative 0; Mismatches 35; Indels 74.
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CATTCGTGATTGCGCCTGAGCGAGAGAATACGCGGATCGCTGTTAAAAGGACAATTACA AACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACC TGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAG TGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAG 4829 CGTCAGCCAGTTTAGTCTGACCATCTCTGTAACATCATTGGCAACGCTACCTTTGCC 4709 TGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA ATTTAATCGCGGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGT -----GGTCGACCAGCCAGTAAGTGAAATCTAGTTCCAA 4440 ACTATTTTGTCATTTTTTAATTTTTCGTATTAGCTTACGACGCTACCACCCCAGTTCCCATCTA CATTCGTGATTGCGCCTGAGCGAGACGAATACGCGATCGCTGTTAAAAGGACAATTACA 4889 TAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCGTAAATTC 4769 ATGTTTCAGAACAACTCTGGCGCATCGGCTTCCCATACAATCGATAGATTGTCGCACC **AATGTAACATCAGAGATTTTTGAGACACACGTGGCTTACTAGGATCCGATATCATTTAAA** TCTAGGGATAACAGGGTAATACTAGTGTCGACCAACCAGATAAGTGAAATCTAGTTCCAA TTTTGTCACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAGTTCCCA TAACCATGCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTC CGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCC ATGITTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACC TGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA **ATTTAATCGCGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGT ATTACTGTTTATGTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGC** ACTATITIGICATITITAATITITCGIATIAGCTIACGACGCIACACCCAGITCCCATCIA 4380 TTTTGTCACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAGTTCCCA DNA sequencing; TnsC transposition regulatory protein; transposase; genetic analysis; gene expression; ds. plasmid pEM delta R.adj

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ACTATITIGICATITITAAITITICGIATIAGCTIACGACGCIACACCCAGIICCCATCIA
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                                              AGGATTATCAATACCATATTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACC
                                                                                            GAGGCAGTTCCATAGGATGCCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAAC
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                                                                                                                                                                                                                                                    The invention relates to a mutant ThsC transposition regulatory protein. This mutant protein activates a transposase in the absence of ThsD or ThsE, which directs intermolecular transposition of a transposable element and discriminates between immune and nonimmune targets, in a manner which is characterised by reduced target site selectivity. It may be used in DNA sequencing methods, for genetic analysis by insertional mutagenesis and alteration of gene expression by insertion of a given penetic sequence. The present DNA sequence is transposon donor plasmid pEM delta R.adj to 1, used in the exemplification of the invention. This plasmid comprises a 1625 bp mini-Th7 element:199 bp of Th7R and 166 bp of Th7L flanking a Kan gene with Sall at the junctions
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5926 BP; 1476 A; 1473 C; 1463 G; 1514 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.7%; Score 1476; DB 6; Length 5926; Best Local Similarity 93.6%; Pred. No. 4.1e-267; Matches 1591; Conservative 0; Mismatches 35; Indels 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTATTAAAGAGGGCGTGGGTCGAC-------
                                                                                                                                                                                    Mutant TnsC transposition regulatory protein for genetic analysis, and alteration of gene given genetic sequence, comprises an alanine
                                                                                                                    JOHNS HOPKINS SCHOOL MEDICINE
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  4440 ACTAITITGICATITITAATITITCGIAITAGCITACGACGCTACACCCAGTICCCAICTA
                            TITIGICACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAGTTCCCA
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Pred. No. 4.1e-267;
0; Mismatches 35;
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                                                                            ACTATTTCTACTCAC 4792
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                                                                                               4320 ACTATTTTGTCGCCCACAC
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Best Local Similarity 93.6%;
Matches 1591; Conservative (
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                                                                                                                                                                                                                                                                                                             Unidentified
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The invention

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GTTATTCATTCGTGATTGCGCCTGAGCGAGACGAATACGCGATCGCTGTTAAAAGGACA 4046
insertional mutagenesis, and alteration of gene expression. The inventior is used to achieve efficient, simple, non-specific or random insertion into any given DNA segment. The present sequence is pEM DNA (pBR plasmid containing a kanamycin mTn7 element) used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAPAGTCTTAAACTAGACAGAATAGTTGTAAACTGAAATCAGTCCGGTTATGCTGTGAAA
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                                                                                             Score 1474; DB 12;
Pred. No. 9.7e-267;
0; Mismatches 40;
                                                                         Sequence 5926 BP; 1475 A; 1471 C; 1464 G; 1516
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                                                                                                             Best Local Similarity 93.3
Matches 1592; Conservative
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                                                                                                                  ACTATTTTGTCATTTTAATTTTCGTATTAGCTTACGACGCTACACCCCAGTTCCCATCTA
                                                                                                                                                                                                                                                           TITIGICACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAGTTCCCA
                                                                                                                                                                                                                                                                                                         TTTGTCACTCTTCCCTAAATAATCCTTAAAAACTCCATTTCCACCCCTCCCAGTTCCA
                 ATTTAATCGCGGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGT
                                                                                                   ATTACTGTTTATGTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGC
                                                                                                                                                 AATGTAACATCAGAGATTTTGAGACACAACGTGGCTTACTAGGATCCGATATCATTTAAA
                                                                                                                                                                                                TCTAGGGATAACAGGGTAATACTAGTGTCGACCAACCAGATAAGTGAAATCTAGTTCCAA
                                                                          ATTTAATCGCGCCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCTTGT
                                                                                                                                                                        The invention relates to a transposon encoding an ATP-utilising regulatory protein containing a mutation that allows efficient and sinsertion of and reduced target site specificity on the transposon. 'invention is used in DNA sequencing methods, for genetic analysis by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprises a mu
reduced target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transposon; ATP-utilising regulatory protein; genetic analysis; insertional mutagenesis; gene; plasmid; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containing a kanamycin mTn7 element)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOHNS HOPKINS SCHOOL MEDICINE
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                                                                                                                                                                                                                                                                                                                                           ACTATTTTCTACTCACTCAC 4792
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specificity on the transposon.
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98US-00027169.
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                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-1997;
20-FEB-1998;
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5072 3686 5012

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Producing heterologous polypeptide by culturing a bacterial cell expressing a fusion protein, comprising a polypeptide with autoproteolytic activity and a heterologous polypeptide, as an inclusion

Example 1; Page 15-17; 31pp; English.

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Knauseder

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Windisch

Stempfer G,

WPI; 2001-191545/19.

(BIOC) BIOCHEMIE GMBH

39-AUG-1999;

07-AUG-2000; 2000WO-EP007643

15-FEB-2001

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The present invention describes a process for the recombinant production of desired heterologous polypeptides (HP). The method comprises culturing a bacterial cell expressing a fusion protein (FP), comprising a colypeptide with autoproteolytic activity of autoprocease Npro and a HP, isolated and treated so that HP is cleaved autoprocease Npro and isolated and treated so that HP is cleaved autoproceolytically by Npro activity from FP. The method is useful for producing a heterologous polypeptide with a clearly defined homogeneous N-terminus in a bacterial, preferably Escherichia coli cell. HP includes enzymes, agents with pharmaceutical activity such as inerleukins, interferons such as leukocyte interferons, growth factors, in particular haemopoietic or wound-healing growth factors, such as granulocyte colony stimulating factor (GCSF), erythropoietin, hormones such as human growth hormone (HGH), antibodies or vaccines The present sequence represents the Nproferon autoprocease and hGH is human growth hormone, which is used in an example
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                                     ATTACAAACAGGAATGGAATGCAACGGCGCAGGAACACTGCCAGGCGCATCAACAATATT
                                                      CGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATATCCCATATAAATCAGCATCCAT
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         GTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACA
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growth hormone;

03-MAY-2001

AAF59457;

RESULT 11

Homo sapiens. Classical swine WO200111057-A1

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Sequence 4840 BP; 1039 A; 1354 C; 1299 G; 1148 T; 0 U; 0 Other;

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The DNA sequence is that of the expression vector pmTNF-MPH which contains the tetracycline resistance gene and origin of replication of pATIS3, the lambda PL promoter up to the MboII site in the N gene 5' untranslated region, followed by a synthetic ribosome binding site and the information encoding the first 25 amino acids of mouse TNF. This sequence is followed by a synthetic polylinker encoding six consecutive histidines followed by several proceolytic sites each accessible via a different restriction enzyme which is unique for the plasmid. Downstream from the polylinker, several transcription terminators are present, including the E. coll trp terminator. The DNA encoding a fragment of the including the E. coll trp terminator. The DNA encoding a fragment of the skpression vector to express the fusion protein mTNF-H6-p362. The
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/note= "rrnBT1T2 contg. HindIII-SepI fragment from
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                                                                                                         pmTNF-MPH plasmid for expression of p362 from M. paratuberculosis.
                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "encodes residues 2-25 of mature mouse
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/note= "HindIII fragment contg. E. coli trp
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/note= "multiple cloning site contg. 6 His
sequence at position 315-332"
                                                                                                                                    Mycobacterium; Crohn's disease; Johne's disease;
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/note= "synthetic DNA fragment"
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purified fusion protein may be used to assay for M. paratuberculosis infections, e.g. Johne's disease in cattle or other animals and possibly Crohn's disease in humans. See also AAQ29145-7. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to correct PI field.)
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Pred. No. 1.2e-261;
0; Mismatches 2;
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2708 2095 2768 2035 Macrophage; induced; lipo-polyasaccharide; antitumour; antiinflammatory; trypanocidal agent; antibody; cell prolification; activation; cytotoxicity; ds. New polypeptide induced in macrophage(s) by lipo-polysaccharide - useful e.g. as antitumour, antiinflammatory or trypanocidal agent, also related 2154 GAATTGGAGCCAATCATTCTTGCGGAGAACTGTGAATGCGCAAACCAAACCAATGGGGGA Van Heuverswyn

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                                                          The plasmid is used to clone and express. The polypeptide induced in macrophages by lipopolysaccharide stimulates cell prolification (esp. when costimulated with IL-4) promote activation, cytotoxicity, and mobilisation of LAK cells; promote recruitment of suppressive peritoneal exudate cells; promote generation of immunocompetent lymph node cells (ILC) and have trypanocidal and trypanolytic activity. The human and murine sequences are given in (AAQS1431-45), peptide fragments able to generate antibodies are given in (AARS1951-61) (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                      Sequence 3474 BP; 845 A; 933 C; 978 G; 718 T; 0 U; 0 Other;
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30.1%; Score 1446.8; DB 2;
Best Local Similarity 99.9%; Pred. No. 1.2e-261;
Matches 1448; Conservative 0; Mismatches 2;
        etc.
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                                   Disclosure; Fig 8b; 108pp; English
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The present invention relates to a method of predicting the evolutionary potential of a mutant resistance gene. The method comprises providing a host cell which includes a mutant resistance gene and determining whether the mutant resistance gene is likely to evolve through two or more and the encoded mutant resistance-conferring polypeptides, and a method of screening a drug for anti-pathogenic activity against a pathogen and assessing the potential longevity of a candidate anti-pathogenic drug. The mutant resistance gene includes two or more nucleic acid assessing the potential longevity of a candidate anti-pathogenic drug. The mutant resistance gene is inserted into a host cell cusing a plasmid and treating the host cell to incorporate the plasmid into the host cell. The method is useful for predicting the evolutionary potential of a mutant resistance gene. The mutant resistance genes are cusful for screening for a drug for anti-pathogenic activity against a pathogen. The present sequence represents a plasmid construct used in the method of the invention.
                                                                                              Predicting the evolutionary potential of a mutant resistance gene, useful for screening for anti-pathogenic drugs comprises determining if a mutant resistance gene is likely to evolve through two or more independent mutation events.
                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1; 47pp; English
                                                  WPI; 2004-313650/29
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Sequence 3801 BP; 939 A; 978 C; 1028 G; 856 T; 0 U; 0 Other;

1388 1448 1508 2129 2189 1568 2069 1628 1748 ö ACCACACCGTCCTGTGGATCCTCTACGCCGGACGCATCGTGGCCGGCATCACCGGCGCC 1889 2009 1688 2008 cecceccaercerecrecerrecerredadecaecrareaceaeracecarcareece 1949 ACAGGTGCGGTTGCTGGCGCCTATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGC 1808 CACTICGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGG 1868 CACTICGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGG 1769 GGACTGTTGGGCGCCATCTCCTTGCATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGC 1928 1329 AATTCTCATGTTTGACAGCTTATCATGGATAAGCTTTAATGCGGTAGTTTATCACAGTTA AATTGCTAACGCAGTCAGGCACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCCTC AATTGCTAACGCAGTCAGGCACCGTGTATGAAATCTAACAATGCGCTCATCGTCATCCTC GCCACCGTCACCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGGTACTGCCGGGCCTC 2188 GGCACCGTCACCCTGGATGCTGTAGGCATAGGCTTGGTTATGCCGGTACTGCCGGGCCTC TTGCGGGATATCGTCCATTCCGACAGCATCGCCAGTCACTATGGCGTGCTGCTAGCGCTA 2128 Treceseararcercearreceacacearceceaercarcareacerarecera TATGCGTTGATGCAATTTCTATGCGCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGC 2068 TATGCGTTGATGCAATTTCTATGCGCACCCGTTCTCGGAGCACTGTCCGACCGCTTTGGC CGCCGCCCAGTCCTGCTTCGCTACTTGGAGCCACTATCGACTACGCGATCATGGČG ACCACACCCGTCCTGTGGATCCTCTACGCCGGACGCATCGTGGCCGGCATCACCGGCGCC Gaps Score 1446.8; DB 12; Length 3801; Pred. No. 1.2e-261; 0; Mismatches 2; Indels 0; C Query Match 30.1%; Best Local Similarity 99.9%; Matches 1448; Conservative (2248 1948 1749 1888 1389 1449 1509 1569 1629 1689 1809 1828 1869 ò 셤 ሯ a ઠે g 8 g 8 8 8 셤 8 6 ⋧ 셤 ò

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g	1708 CTCA	ACCTACTACTGGGGTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGGGTCGACCG 1649
ò	1989 ATGC	ATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCGGTGGGCGCGGGGCATGACTATC 2048
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ò	69	SGIATTCGGATCTTGCACGCCTCGCTCAAGCCTTCGTCACTGGTCCCGCCACC 222
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ò	2349 TCCGC	GGCGGCATCGGGATGCCCGCGTTGCAGGCCATGCTGTCCAGGCAGG
đ	1288 TCCGC	GGGCATCGGGATGCCCGCGTTGCAGGCCATGCTGTCCAGGCAGG
ò	2409 CATC	CATCAGGGACAGCTTCAAGGATGCTCGCGGCTCTTACCAGCCTAACTTCGATCATTGGA 2468
qq	1228 CATC	
ò	2469 CCGCT	CCGCTGATCGTCACGGCGATTTATGCCGCCTCGGCGAGCACACAGGAACGGGTTGGCATGG 2528
g	1168 CCGC	IGATCGTCACGGCGATTTATGCCGCCTCGGCGACACGCAATGGAACGGGTTGGCATGG 1109
δλ	2529 ATTG1	TAGGGCCCCCTATACCTTGTCTGCCTCCCGGGTTGCGTGCG
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pACYC184; origin
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5.1.6 Compugen Ltd.	; Search time 20375.3 Seconds (without alignments) 11054.239 Million cell updates/sec	.taagatgctttctgtgact 4814	90	8: 82156650					cted by chance to have a cof the result being printed, score distribution.		Description	BZ430219 BONDÄ17FF BZ430224 BONDÄ17TR AZ682163 ENTIW91TR AL419357 T7 end of CF577494 AGENCOURT BH600610 BOHKÒ87IF	CG411076 KM31 LXX AJ762384 AJ762384 AJ762542 AJ762538 BF632491 NF027F11D BQ752029 BST632592 CG304998 111R05681	BJ684207 BJ684207 BJ683711 BJ683711 BJ683533 BJ683533 BJ683290 BJ683290 BJ683026 BJ683026 BH146743 ENTPJ23TF	BJ684301 BJ684301 BJ683987 BJ683987 AZS41608 ENTFU74TF BJ682782 BJ682782
GenCore version 5.1 Copyright (c) 1993 - 2006 CompOM THE COMPANSION OF THE COMPANSION OF THE CONTRACT OF THE C	January 17, 2006, 18:09:28	7-7 gaatgcgcaa	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 41078135 segg 23193541228 regidines	mber of hits satisfying	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:* 1: 9b est1:* 2: 9b_est2:* 3: 9b_est3:* 4: 9b htc:* 5: 9b_est4:* 6: 9b_est5:* 7: qb_est6:*		Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score di	SUMMARIES	Result Query No. Score Match Length DB ID		658 13.7 663 10 648 13.5 648 1 646 13.4 659 2 645 13.4 659 2 645 13.4 659 5 645 13.4 681 15	13 641 13.3 675 14 641 13.3 676 15 637.4 13.2 683 16 636.4 13.2 675 17 636.4 13.2 675 18 635.4 13.2 945	635 13.2 651 3 635 13.2 670 3 628.4 13.1 947 9 627.6 13.0 643 3

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BZ430224 BDNDX17TR BO_1.6_2_KB_tot Brassica oleracea genomic clone BONDX17, genomic survey sequence.
BZ430224.1 GI:26675106

DEFINITION ACCESSION VERSION

RESULT 2 BZ430224

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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using BstXI linkers"
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                                                                                           Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-838-3523
Fax: 301-838-0208
Email: cdcwn@tigr.org
DNA is from a doubled haploid provided by Tom Os Seg primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="BO_1.6_2 KB_tot"
/note="Vector: pHOS1; Site_1:
total DNA inserted into pHOS1
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/organism="Brassica oleracea"
/wol type="genomic DNA"
/strain="TO1000DH3"
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/clone="BONDX17"
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Contact: Chris Town
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Best Local Similarity 100.
Matches 918; Conservative
Brassica oleracea
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/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOSI, Site_1: Bet I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
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BNT1M91TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.

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    /organism="Entamoeba histolytica"

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1 (bases 1 to 881)

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from this in the second of clone end sequences from the information of clone end sequences from the information of Eukaryotic Genomics of the Institute for Genomic Research 120 in 181 81 80 208

Fax: 301 838 3543
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/strain="HM1:IMSS"
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High quality sequence start: 17
High quality sequence stop: 816.
Location/Qualifiers
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Clones are derived from the
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77:450.). The DNA was mechanically sheared to give a tright size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Ly Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 31057 BYRY cedex, FRANCE. (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida troplicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
                                                                                                                                                                      SM Pichia farinosa

Sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.

Saccharomycetales; Saccharomycetaceae; Pichia.

E 1 (bases 1 to 988)

S Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Brottler,P., Casaregla,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Winncker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
L FEBS Lett. 487 (1), 3-12 (2000)
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                                end of clone AXOAA038H01 of library AXOAA from strain CBS 7064 Pichia farinosa, genomic survey sequence.
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de Montigny,J., Spehner,C., Souciet,J., Tekaia,F., Dujon,B.,
Wincker,P., Artiguenave,F. and Potier,S.
Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
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Pred. No. 7.3e-190;
2; Mismatches 5;
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strain="CBS 7064"
/db_xref="texon:4920"
/clone="AxOAA038H01"
/clone lib="AXOAA3
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al Similarity 99.0%;
721; Conservative
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AGENCOURT 112111379_updated NIH_MGC_137 Mus musculus cDNA clone LEST 24-SEB-2003 LIMAGE.6436303 5', mRNA sequence.
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
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                              441 AATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATG
                                                                                                                                           3936 AACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCAT
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                                                                                                                3876 AGTGACGACTGAATCCGGTGAGAATGGCAAAAGCTTATGCATTTCCTTTCCAGACTTGTTC
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloApd? Bethada, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
CDNA Library Preparation: Catherine Lee, Endocrine Pancreas
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BH600610 675 bp DNA linear GSS 15-DEC-2001
BOHKQB1TF BOHK Brassica oleracea genomic clone BOHKQB7, genomic
BUTYOEy sequence.
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Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback, T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
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/clone="BOHKOB7"
/clone lib="BOHK"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by Tom Osborn
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Pred. No. 3.8e-176;
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/organism="Brassica oleracea"
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Tel: 301-838-3523
Fax: 301-838-0208
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/strain="TO1000DH3"
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DNA is from a doubled ha
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Class: sheared ends.
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quality sequence start: 16 quality sequence stop: 627. Location/Qualifiers
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LOCUS DEFINITION

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ACCESSION VERSION KEYWORDS ORGANISM

AUTHORS REFERENCE

TITLE

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mRNA linear EST 03-JUN-2005
'Terra Regina' cDNA clone
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Gerbera hybrid cv. 'Terra Regina'
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Mutisioideae,
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I (basea 1 to 648)
Lattinen,R.A. Immanen,J., Auvinen,P., Rudd,S., Alatalo,E.R.,
Paulin,L., Ainasoja,M., Kotilainen,M., Koskela,S., Teeri,T.H. and
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    .648
    /organism="Gerbera hybrid

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/clone="G0000600011D12F1"
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/cultivar="Terra Regina"
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Viikinkaari 9, P.O. Box 56, 0
Location/Qualifiers
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/mol_type="genomic DNA"
/sub_species="xyli"
/sub_species="xyli"
/db xref="texxon:5973"
/clone_lib="Lxx transposon mutant library"
/note="Vector: pUCD623; Lxx transposon mutants were
generated by electroporating pUCD623 containing the
transposon T14431 into Lxx cells grown from 10-15 days
S8 broth containing 0.1% glycine."
                                                                                                                                                                                                                                                                                                                               GACCGCTGATCGTCACGGCGATTTATGCCGCCCTCGGCGACACATGGAACGGGTTGGCAT
                                                                GACCGCTGATCGTCACGCCGATTTTATGCCGCCTCGGCGAGCACATGGAACGGGTTGGCAT
                                                                                                                                               GGATTGTAGGCGCCGCCCTATACCTTGTCTGCCTCCCCGCGTTGCGTCGCGTGCATGGA
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Leifsonia xyli subsp. xyli
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Microbacteriaceae; Leifsonia.
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Brumbley,S.M., Petrasovits,L.A., Murphy,R.M., Nagel,R.J.,
Candy,J.M. and Hermann,S.R.
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50 Meiers Rd, Indoorcopilly, Brisbane, 4068, Australia

Tel: 61 7 331 333

Fax: 61 7 3871 0383

Fax: 61 7 3871 0383

Email: sbrumbley@bses.org.au

Class: transposon insertion site.
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Mol. Plant Microbe Interact. 17 (2), 175-183 (2004)
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DNPRC
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of Helsinki, FINLAND.

ORIGIN

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NF027F11DT1F1092 Drought Medicago truncatula cDNA clone NF027F11DT 5', mRNA sequence.
BF632491.1 GI:11896649
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                                                                                                                                                            'Terra Regina'
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  differentiation in Gerbera hybrida (Asteraceae)
Genome Res. 15 (4), 475-486 (2005)
                                                                                                  00014 University
                                                                                                                                                                                                                                                                                                                                  Query Match 13.5%; Score 648; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.5e-170;
Matches 648; Conservative 0; Mismatches 0;
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/organism="Gerbera hybrid c"
/mol_type="mRNA"
/cultivar="Terra Regina"
/db_xref="texon:226891"
/clone="G0000600013D05F1"
                                                                                                                                                                                                                                                        /tissue_type="flower stem"/clone_lib="G00006"
                                                                              Institute of Biotechnology
Viikinkaari 9, P.O. Box 56, 0
Location/Qualifiers
                                          15781570
Contact: Alatalo ER
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Gerbera hybrid cv. 'Terra Regina'
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Mutisioideae;
Mutisieae; Gerbera.
I (bases 1 to 648)
Laitinen, R.A., Immanen, J., Auvinen, P., Rudd, S., Alatalo, B.R.,
Paulin, L., Ainasoja, M., Kotilainen, M., Koskela, S., Teeri, T.H. and
Elomaa, P.
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G0000600013D05F1, mRNA sequence.
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                                                                              Length 648;
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                                                                          13.5%; Score 648; DB 1; Le
100.0%; Pred. No. 6.5e-170;
ive 0; Mismatches 0;
/tissue_type="flower stem"
/clone_lib="G00006"
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minimal medium
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DSCT Colletotrichum trifolii cDNA clone pDSCT9-44, mRNA
1867
                                                                                                                                  GGGACTGTTGGGCGCCATCTCCTTGCATGCACCATTCCTTGCGGCGGCGGGGGTGCTCAACGG 1927
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                                                               540
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1 (bases 1 to 645)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.

ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
                                                                                                                                                                                                                                                                                                               available at:
                                   481 CCACTTCGGGCTCCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGG
CCACTTCGGGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGG
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/dev stage="Young, actively growing mycelia
inocilation) grown in liquid culture (cutin lonearianing 2%glucose)."
/lab_host="DHSalpha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSA144TV More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          495 Borlaug Hall, 1991 Upper Buford Circle, St.
Tel: 612 625 1243
Fax: 651 649 5058
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Seg primer: (grA AtA CgA CtC ACt AtA ggg '
Location/Qualifiers
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/clone="pDSCT9-44"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
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/strain="race 1"
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Colletotrichum trifolii
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
Unpublished (2000)
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/dev_stage="Pooled timepoints"
/clone_lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entix
/note="Vector: Lambda in a series of days-post-watering
timepoints."
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Plant Biology Division
The Samuel Roberts Noble Foundation
The Sam Noble Parkway, Ardmore, OK 73402, USA
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Location/Qualifiers
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/organism="Zea mays"
/mol type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db xref="taxon:4577"
/db xref="taxon:4577"
/dev_stage="adult"
/lab_host="blu08"
/clone_lib="ll18 - RescueMu Grid S"
/note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid S was grown at San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1825
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Pred. No. 1.7e-168;
0; Mismatches 5;
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99.0%;
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6

GCCCGCGTTGCAGCC

1935

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546

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BJ683711 HCEST library Haplochromis chilotes cDNA clone no86a05,
                                                                                                                                GGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGGGGACTGT 1875
                                                                                                                                                                                                                                                                               1936 TACTACTGGGCTGCTTCCTAATGCAGGAGTCGCATAAGGGAGAGCGTCGACCGATGCCCT 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natanabe, M., Kobayashi, N., Shin-i, T., Horiike, T., Tateno, Y., Kohara, Y. and Okada, N. Kohara, Y. and Okada, N. Statensive analysis of ORF sequences from two different cichlid species in Lake Victoria provides molecular evidence for a recent radiation event of the Victoria species flock: identity of EST gequences between Haplochromis chilotes and Haplochromis sp. Gene 343 (2), 263-269 (2004)
1336 ATGTTTGACAGCTTATCATCGATAAGCTTTAATGCGGTAGTTTATCACAGTTAAATTGCT
                                                                                               427 CGGTTGCTGGCGCCTATATCGCCGACATCACCGATGGGGAAGATCGGGCTCGCCACTTCG
                                                                                                                                                            487 GGCTCATGAGCGCTTGTTTCGGCGTGGGTATGGTGGCAGGCCCCCGTGGCCGGGGAACTGT
                                                                                                                                                                                                        TGGGCGCCATCTTGCATGCACCATTCCTTGCGGCGGCGGTGCTCAACGGCCTCAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Pax: 81-559-81-6855
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/dev stage="varied"
/clone lib="HCEST library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Haplochromis
/mol_type="mRNA"
/db_xref="taxon:257977"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="no86a05"
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Haplochromis chilotes
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Matches 65
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidea; African cichlids; Pseudocrenilabrinae;
Haplochromin; Haplochromis.

E 1 (bases 1 to 675)
Watanabe, M., Kobayashi, N., Shin-i, T., Horiike, T., Tateno, Y.,
Kohara, Y. and Okada, N.
Extensive analysis of ORF sequences from two different cichlid
species in Lake Victoria provides molecular evidence for a recent
radiation event of the Victoria species flock: identity of EST
sequences between Haplochromis chilotes and Haplochromis sp.
1 Gene 313 (2), 263-269 (2004)
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                                                                                BJ684207 BJ684207 HCEST library Haplochromis chilotes cDNA clone no90g11,
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Haplochromis chilotes"
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llarity 98.4%; Pred. No. 6.1e-168;
Conservative 0; Mismatches 10;
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/db_xref="taxon:257977"
/clone="no90g11"
/tissue_type="jaw"
/dev_stage="varied"
/clone_lib="HGEST library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                       BJ684207.1 GI:46527328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tadasu Shin-i
                                                                                                                                                                                             Haplochromis chilotes
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Pred. No. 6.3e-167;
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98.3%; Pred. No. b...
... 0; Mismatches
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/dev_stage="varied"
/clone_lib="HCEST_library"
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organism="Haplochromis"
                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:257977"
/clone="no82a09"
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1111 Yata, Mishima, Shizuoka 4
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostcmi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Acanthomorpha; African cichlids; Pseudocrenilabrinae;
Haplochromnii; Haplochromis.

E 1 (bases 1 to 683)
S Watanabe, M. Kobayashi, N., Shin-i, T., Horiike, T., Tateno, Y., i

Kohara, Y. and Okada, N.

Extensive analysis of ORF sequences from two different cichlid

Extensive analysis of ORF sequences from two different cichlid

Species in Lake Victoria provides molecular evidence for a recent
radiation event of the Victoria species flock: identity of E&F

Sequences between Haplochromis chilotes and Haplochromis sp.
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